

WEST Search History

DATE: Thursday, May 12, 2005

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<input type="checkbox"/>	L3	botulin or botulinum or botinolysin or botulism or botox or btx or neurotoxin or neuro-toxin	11128
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<input type="checkbox"/>	L6	(l1 or l2).clm. and l3.clm.	31

END OF SEARCH HISTORY

WEST Search History

DATE: Thursday, May 12, 2005

Hide? Set Name Query Hit Count

DB=PGPB; PLUR=YES; OP=AND

<input type="checkbox"/>	L1	20030009025	1
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END OF SEARCH HISTORY

Hit List

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Search Results - Record(s) 1 through 1 of 1 returned.

1. Document ID: US 20030009025 A1

L6: Entry 1 of 1

File: PGPB

Jan 9, 2003

DOCUMENT-IDENTIFIER: US 20030009025 A1

TITLE: Recombinant vaccine against botulinum neurotoxin

Pre-Grant Publication (PGPub) Document Number:

20030009025

Summary of Invention Paragraph:

[0008] Human botulism poisoning is generally caused by type A, B, E or rarely, by type F toxin. Type A and B are highly poisonous proteins which resist digestion by the enzymes of the gastrointestinal tract. Foodborne botulism poisoning is caused by the toxins present in contaminated food, but wound and infant botulism are caused by in vivo growth in closed wounds and the gastrointestinal tract respectively. The toxins primarily act by inhibiting the neurotransmitter acetylcholine at the neuromuscular junction, causing paralysis. Another means for botulism poisoning to occur is the deliberate introduction of the toxin(s) into the environment as might occur in biological warfare. When the cause of botulism is produced by toxin rather than by in vivo infection the onset of neurologic symptoms is usually abrupt and occurs within 18 to 36 hours after ingestion. The most common immediate cause of death in respiratory failure due to diaphragmatic paralysis. Home canned foods are the most common sources of toxins. The most frequently implicated toxin is toxin A, which is responsible for more than 50% of morbidity resulting from botulinum toxin.

Summary of Invention Paragraph:

[0010] Agents that abolish the action of BoNT have been investigated since the 1940s. Early work at Fort Detrick in the 1940s lead to the development of a toxoid vaccine to protect against serotypes A, B, C.sub.1, D, and E toxins. The toxoid vaccine was manufactured by growing five Clostridium botulinum strains, extracting and precipitating the toxin from the growth media after cell lysis. Formalin was added to the crude preparation to inactivate the neurotoxin. Residual formalin was left in the vaccine product to ensure the toxin remains non-toxic. The product was adsorbed to aluminum hydroxide and blended. Currently, a pentavalent toxoid vaccine against serotypes A through E (Anderson, J. H., et al., (1981), "Clinical Evaluation of Botulinum Toxoids," Biomedical Aspects of Botulism, (Lewis, G. E., Ed.), pp. 233-246, Academic Press, New York; Ellis, R. J., (1982), "Immunobiologic Agents and Drugs Available from the Centers for Disease Control. Descriptions, Recommendations, Adverse Reactions and Serologic Response," 3rd ed., Centers for Disease Control. Atlanta, Ga.; Flock, M. A., et al., (1963), "Studies of Immunities to Toxins of Clostridium Botulinum. IX. Immunologic Response of Man to Purified Pentavalent ABCDE Botulinum Toxoid," J. Immunol., 90:697-702; Siegel, L. S., (1988), "Human Immune Response to Botulinum Pentavalent (ABCDE) Toxoid Determined by a Neutralization Test and by an Enzyme-Linked Immunosorbent Assay," J. Clin. Microbiol., 26:2351-2356), available under Investigational New Drug (IND) status,

is used to immunize specific populations of at-risk individuals, i.e., scientists and health care providers who handle BoNT and our armed forces who may be subjected to weaponized forms of the toxin. Though serotypes A, B, and E are most associated with botulism outbreaks in humans, type F has also been diagnosed (Midura, T. F., et al., (1972), "Clostridium botulinum Type F: Isolation from Venison Jerky," Appl. Microbiol. 24:165-167; Green, J., et al., (1983), "Human Botulism (Type F)--A Rare Type," Am. J. Med., 75:893-895; Sonnabend, W. F., et al., (1987), "Intestinal Toxicoinfection by Clostridium botulinum Type F in an Adult. Case Associated with Guillain-Barre Syndrome," Lancet, 1:357-361; Hatheway, C. L., (1976), "Toxoid of Clostridium botulinum Type F: Purification and Immunogenicity Studies," Appl. Environ. Microbiol., 31:234-242). A separate monovalent toxoid vaccine against BoNTF is available under IND status. Hatheway demonstrated that the BoNTF toxoid could protect guinea pigs against a homologous challenge (Wadsworth, J. D. F., et al., (1990), "Botulinum Type F Neurotoxin," Biochem. J., 268:123-128).

Detail Description Paragraph:

[0063] The synthetic gene for BoNT serotype B fragment H.sub.C (see FIG. 4A) has been inserted into the yeast expression vector PHIL-D4, and integrated into the chromosome of *Pichia pastoris* strain GS115. The expressed product (see amino acid sequence in FIG. 4B) had the expected molecular weight as shown by denaturing polyacrylamide gel electrophoresis (PAGE) and Western blot analysis using antibodies directed against botulinum neurotoxin serotype B. The expressed recombinant BoNTB (H.sub.C) elicited high antibody titers as judged by the Enzyme Linked Immunosorbent Assay (ELISA) and, more importantly, these circulating serum titers protected mice, guinea pigs, and non-human primates from challenges with active toxin. Industrial scale manufacturing processes (fermentation and purification) have been completed and a pilot lot has been produced in compliance with cGMP.

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L1 and human	1

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US-PAT-NO: 5939070

DOCUMENT-IDENTIFIER: US 5939070 A

TITLE: Hybrid botulinal neurotoxins

DATE-ISSUED: August 17, 1999

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Johnson; Eric A.	Madison	WI		
Goodnough; Michael C.	Stoughton	WI		
Bradshaw; Marite	Madison	WI		

US-CL-CURRENT: 424/194.1, 424/239.1, 435/220, 435/842, 514/12, 530/350, 530/402, 530/412,
530/825, 536/23.2, 536/23.7

CLAIMS:

We claim:

1. A hybrid botulinal neurotoxin comprising:

- (a) a botulinal neurotoxin light chain; and
- (b) a botulinal neurotoxin heavy chain,

wherein the light chain and heavy chain are not of the same serotype and wherein the light and heavy chains are linked by a heterobifunctional thiol/amine linker and wherein the specific toxicity of the neurotoxin is at least 10.^{sup.6} LD._{sub.50} /mg protein in vivo.

2. The neurotoxin of claim 1 wherein the heavy chain or light chain is isolated from a native botulinal neurotoxin molecule.

3. The neurotoxin of claim 1 wherein the heavy chain or light chain is obtained from a recombinant gene construct.

4. The neurotoxin of claim 1 wherein the heavy and light chains are obtained from recombinant gene constructs.

5. A hybrid botulinal neurotoxin comprising light and heavy chains, which comprise botulinal neurotoxin catalytic, channel forming and receptor binding functional domains, wherein at least two functional domains are from botulinal neurotoxins of different serotypes and wherein the light and heavy chains are linked by a heterobifunctional thiol/amine linker and wherein the specific toxicity of the neurotoxin is at least 10.^{sup.6} LD._{sub.50} /mg protein in vivo.

6. The neurotoxin of claim 5 wherein at least one of the functional domains is isolated from a native botulinal neurotoxin molecule.

7. The neurotoxin of claim 5 wherein at least one of the functional domains is isolated from a recombinant gene construct.

8. The neurotoxin of claim 5 wherein the heavy and light chains are obtained from recombinant gene constructs.

9. A pharmaceutical composition comprising the neurotoxin of claim 1.

10. A pharmaceutical composition comprising the neurotoxin of claim 5.

11. A method for creating a hybrid neurotoxin comprising the steps of:

(a) isolating botulinal neurotoxin heavy and light chains from native neurotoxin molecules or a recombinant gene construct; and

linking the heavy and light chains into a hybrid neurotoxin with a heterobifunctional thiol/amine linker wherein the heavy and light chains are not of the same serotype and wherein the specific toxicity of the neurotoxin is at least 10.^{sup.6} LD._{sub.50} /mg protein *in vivo*.

12. The method of claim 11 wherein the heavy and light chains are obtained from recombinant gene constructs.

13. The method of claim 12 wherein the recombinant gene constructs encode combinations of functional domains that do not occur naturally.

14. A hybrid neurotoxin created by the method of claim 13.

L6: Entry 23 of 31

File: USPT

Mar 30, 2004

US-PAT-NO: 6713444

DOCUMENT-IDENTIFIER: US 6713444 B1

TITLE: Buforin I as a specific inhibitor and therapeutic agent for botulinum toxin B and tetanus neurotoxins

DATE-ISSUED: March 30, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Garcia; Gregory E.	Germantown	MD		
Gordon; Richard K.	Potomac	MD		
Moorad; Debbie R.	Rockville	MD		
Doctor; Bhupendra P.	Potomac	MD		

US-CL-CURRENT: 514/2; 424/239.1, 424/9.1, 435/252.7, 514/13, 514/21, 530/324, 530/326, 530/333, 530/344

CLAIMS:

What is claimed is:

1. A pharmaceutical composition for treating botulinum or tetanus toxin poisoning which comprises a biocompatible chaotropic and an endoprotease inhibiting amount of a compound selected from the group consisting of

AlaGlyArgGlyLysGlnGlyGlyLysValArgAlaLysAlaLysThrArgSerSerArgAlaGlyLeuGlnPhe
Pro ValGlyArgValHisArgLeuLeuArgLysGlyAsnTyr (SEQ ID NO:1)

ThrArgSerSerArgAlaGlyLeuGlnPheProValGlyArgValHisArgLeuLeuArgLys (SEQ ID NO:2),

ThrArgSerSerArgAlaGlyLeuGlnPheProValGlyArgValHisArgLeuLeuArgLysGlyAsnTyr (SEQ ID NO:3),

AlaGlyArgGlyLysGlnGlyGlyLysValArgAlaLysAlaLysThrArgSerSerArgAlaGlyLeuGlnPhe
Pro ValGlyArgValHisArgLeuLeuArgLys (SEQ ID NO:4) and the amidated forms thereof.

2. The pharmaceutical composition of claim 1, wherein the purified and isolated form is a phosphate salt.

3. The pharmaceutical composition of claim 2, wherein the phosphate salt is formed by the phosphorylation of Ser, Thr or Tyr.

4. The pharmaceutical composition of claim 1, further comprising tris-(2-carboxyethyl) phosphine (TCEP).

5. The pharmaceutical composition of claim 1, wherein the biocompatible chaotrope is hydroxyurea or 2-oxo-1 pyrrolidine acetamide.

6. A method for treating botulinum or tetanus toxin poisoning comprising administering to a subject suspected of having botulinum or tetanus toxin poisoning an amount of a compound for a time and under conditions effective to inhibit the toxin poisoning, wherein the compound is selected from the group consisting of

AlaGlyArgGlyLysGlnGlyGlyLysValArgAlaLysAlaLysThrArgSerSerArgAlaGlyLeuGlnPhe
Pro ValGlyArgValHisArgLeuLeuArgLysGlyAsnTyr (SEQ ID NO:1),

ThrArgSerSerArgAlaGlyLeuGlnPheProValGlyArgValHisArgLeuLeuArgLys (SEQ ID NO:2),

ThrArgSerSerArgAlaGlyLeuGlnPheProValGlyArgValHisArgLeuLeuArgLysGlyAsnTyr (SEQ ID NO:3),

AlaGlyArgGlyLysGlnGlyGlyLysValArgAlaLysAlaLysThrArgSerSerArgGlyLeuGlnPhePro
ValGlyArgValHisArgLeuLeuArgLys (SEQ ID NO:4),

ThrArgAlaArgAlaGlyLeuGlnPheProValGlyArgValHisArgLeuLeuArgLys (SEQ ID NO:5),

ThrArgLeuLeuArgAlaGlyLeuGlnPheProValGlyArgValHisArgLeuLeuArgLys (SEQ ID NO:6),

and the amidated forms thereof.

7. The method of claim 6, wherein the compound is administered to the subject prior to the subjects contact with Botulinum or tetanus intoxication.

8. The method of claim 7, wherein the Botulinum or tetanus intoxication results from aerosol contamination.

9. The method of claim 8, wherein the administration involves impregnating a filter with the compound and affixing it to the subject.

10. The method of claim 9, wherein the filter is a breathing filter.

11. The method of claim 6, wherein the compound is administered directly to a wound on the subject.

12. The method of claim 6, wherein the compound is conjugated to botulinum toxin heavy chain (Btx-HC).

Day : Thursday
Date: 5/12/2005

Time: 14:31:36

 PALM INTRANET**Application Number Information**Application Number: **10/729122****Assignments**Filing or 371(c) Date: **12/05/2003**Effective Date: **12/05/2003**Application Received: **12/08/2003**Pat. Num./Pub. Num: **/20040115215**Issue Date: **00/00/0000**Date of Abandonment: **00/00/0000**Attorney Docket Number: **D-
2939CIPCONDIV2**Status: **41 /NON FINAL ACTION MAILED**Confirmation Number: **9828**Examiner Number: **72798 /PORTNER, GINNY**Group Art Unit: **1645 IFW IMAGE**

Class/Subclass:

424/130.100Lost Case: **NO**

Waiting for Response

Interference Number:

Desc.

Mail Non FinalUnmatched Petition: **NO****L&R Code:** Secrecy Code:1Third Level Review: **NO**Secrecy Order: **NO**Status Date: **02/10/2005**Oral Hearing: **NO**Title of Invention: **RECOMBINANT BOTULINUM TOXINS WITH A SOLUBLE C-TERMINAL PORTION, AN N-TERMINAL PORTION AND A LIGHT CHAIN**

Bar Code	PALM Location	Location Date	Charge to Loc	Charge to Name	Employee Name	Location
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Appln Info	Contents	Petition Info	Atty/Agent Info	Continuity Data	Foreign Data	Inv
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Pro Phe Asp Phe Lys Leu Gly Ser Ser Gly Glu Asp Arg Gly Lys Val
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Entry information

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Secondary accession number	P10843
Entered in Swiss-Prot in	Release 11, July 1989
Sequence was last modified in	Release 26, July 1993
Annotations were last modified in	Release 47, May 2005
Name and origin of the protein	
Protein name	Botulinum neurotoxin type B [Precursor]
Synonyms	EC 3.4.24.69 BoNT/B Bontoxilysin B
Gene name	Name: botB
From	Clostridium botulinum [TaxID: 1491]
Taxonomy	Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.

References

[1] NUCLEOTIDE SEQUENCE.

MEDLINE=92384550;PubMed=1514783 [NCBI, ExPASy, EBI, Israel, Japan]
 Whelan S.M., Elmore M.J., Bodsworth N.J., Brehm J.K., Atkinson T., Minton N.P.;
 "Molecular cloning of the Clostridium botulinum structural gene encoding the type B neurotoxin
 and determination of its entire nucleotide sequence.";
Appl. Environ. Microbiol. 58:2345-2354(1992).

[2] NUCLEOTIDE SEQUENCE OF 35-245.

STRAIN=Type B / NCTC 7273;
 Szabo E.A., Pemberton J.M., Desmarchelier P.M.;
 Submitted (APR-1992) to the EMBL/GenBank/DDBJ databases.

[3] NUCLEOTIDE SEQUENCE OF 633-993.

STRAIN=Type B / NCTC 7273;
 MEDLINE=94013372;PubMed=8408542 [NCBI, ExPASy, EBI, Israel, Japan]
 Campbell K.D., Collins M.D., East A.K.;
 "Gene probes for identification of the botulinal neurotoxin gene and specific identification of
 neurotoxin types B, E, and F.";
J. Clin. Microbiol. 31:2255-2262(1993).

[4] PROTEIN SEQUENCE OF 1-44 AND 441-466.

STRAIN=Type B / B-657;

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References

[1] NUCLEOTIDE SEQUENCE.

MEDLINE=92384550;PubMed=1514783 [NCBI, ExPASy, EBI, Israel, Japan]
 Whelan S.M., Elmore M.J., Bodsworth N.J., Brehm J.K., Atkinson T., Minton N.P.;
 "Molecular cloning of the Clostridium botulinum structural gene encoding the type B neurotoxin
 and determination of its entire nucleotide sequence.";
Appl. Environ. Microbiol. 58:2345-2354(1992).

[2] NUCLEOTIDE SEQUENCE OF 35-245.

STRAIN=Type B / NCTC 7273;
 Szabo E.A., Pemberton J.M., Desmarchelier P.M.;
 Submitted (APR-1992) to the EMBL/GenBank/DDBJ databases.

[3] NUCLEOTIDE SEQUENCE OF 633-993.

STRAIN=Type B / NCTC 7273;
 MEDLINE=94013372;PubMed=8408542 [NCBI, ExPASy, EBI, Israel, Japan]
 Campbell K.D., Collins M.D., East A.K.;
 "Gene probes for identification of the botulinal neurotoxin gene and specific identification of
 neurotoxin types B, E, and F.";
J. Clin. Microbiol. 31:2255-2262(1993).

[4] PROTEIN SEQUENCE OF 1-44 AND 441-466.

STRAIN=Type B / B-657;

DOI=10.1016/0300-9084(88)90111-3; MEDLINE=89000987; PubMed=3139097 [NCBI, ExPASy, EBI, Israel, Japan]
 Dasgupta B.R., Datta A.;
 "Botulinum neurotoxin type B (strain 657): partial sequence and similarity with tetanus toxin."; Biochimie 70:811-817(1988).

[5] PROTEIN SEQUENCE OF 1-16 AND 441-458.

STRAIN=Type B / Okra;
 MEDLINE=85197963; PubMed=3888113 [NCBI, ExPASy, EBI, Israel, Japan]
 Schmidt J.J., Sathyamoorthy V., Dasgupta B.R.;
 "Partial amino acid sequences of botulinum neurotoxins types B and E."; Arch. Biochem. Biophys. 238:544-548(1985).

[6] IDENTIFICATION AS ZINC-PROTEASE.

MEDLINE=93054694; PubMed=1429690 [NCBI, ExPASy, EBI, Israel, Japan]
 Schiavo G., Rossetto O., Santucci A., Dasgupta B.R., Montecucco C.;
 "Botulinum neurotoxins are zinc proteins."; J. Biol. Chem. 267:23479-23483(1992).

[7] IDENTIFICATION OF SUBSTRATE.

DOI=10.1038/359832a0; MEDLINE=93063293; PubMed=1331807 [NCBI, ExPASy, EBI, Israel, Japan]
 Schiavo G., Benfenati F., Poulaing B., Rossetto O., de Laureto P.P., Dasgupta B.R., Montecucco C.;
 "Tetanus and botulinum-B neurotoxins block neurotransmitter release by proteolytic cleavage of synaptobrevin."; Nature 359:832-835(1992).

Comments

- **FUNCTION:** Botulinum toxin acts by inhibiting neurotransmitter release. It binds to peripheral neuronal synapses, is internalized and moves by retrograde transport up the axon into the spinal cord where it can move between postsynaptic and presynaptic neurons. It inhibits neurotransmitter release by acting as a zinc endopeptidase that cleaves the 76-Gln- β -Phe-77 bond of synaptobrevin-2.
- **CATALYTIC ACTIVITY:** Limited hydrolysis of proteins of the neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No detected action on small molecule substrates.
- **COFACTOR:** Binds 1 zinc ion per subunit (*By similarity*).
- **SUBUNIT:** Disulfide-linked heterodimer of a light chain (L) and a heavy chain (H). The light chain has the pharmacological activity, while the N- and C-terminal of the heavy chain mediate channel formation and toxin binding, respectively.
- **SUBCELLULAR LOCATION:** Secreted.
- **MISCELLANEOUS:** There are seven antigenically distinct forms of botulinum neurotoxin: Types A, B, C1, D, E, F, and G.
- **SIMILARITY:** Belongs to the peptidase M27 family [view classification].

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Cross-references

EMBL	M81186; AAA23211.1; -;	[EMBL / GenBank / DDBJ]
	Genomic_DNA.	[CoDingSequence]
	Z11934; CAA77991.1; -;	[EMBL / GenBank / DDBJ]
	Genomic_DNA.	[CoDingSequence]
	X70817; CAA50148.1; -;	[EMBL / GenBank / DDBJ]
	Genomic_DNA.	[CoDingSequence]

DOI=10.1016/0300-9084(88)90111-3; MEDLINE=89000987; PubMed=3139097 [NCBI, ExPASy, EBI, Israel, Japan]
 Dasgupta B.R., Datta A.;
 "Botulinum neurotoxin type B (strain 657): partial sequence and similarity with tetanus toxin."; Biochimie 70:811-817(1988).

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 "Partial amino acid sequences of botulinum neurotoxins types B and E."; Arch. Biochem. Biophys. 238:544-548(1985).

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 "Botulinum neurotoxins are zinc proteins."; J. Biol. Chem. 267:23479-23483(1992).

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- **SUBUNIT:** Disulfide-linked heterodimer of a light chain (L) and a heavy chain (H). The light chain has the pharmacological activity, while the N- and C-terminal of the heavy chain mediate channel formation and toxin binding, respectively.
- **SUBCELLULAR LOCATION:** Secreted.
- **MISCELLANEOUS:** There are seven antigenically distinct forms of botulinum neurotoxin: Types A, B, C1, D, E, F, and G.
- **SIMILARITY:** Belongs to the peptidase M27 family [view classification].

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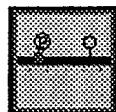
Cross-references

EMBL	M81186; AAA23211.1; -;	[EMBL / GenBank / DDBJ]
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	Z11934; CAA77991.1; -;	[EMBL / GenBank / DDBJ]
	Genomic_DNA.	[CoDingSequence]
	X70817; CAA50148.1; -;	[EMBL / GenBank / DDBJ]
	Genomic_DNA.	[CoDingSequence]

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	1EPW; X-ray; A=1-1290. [ExPASy / RCSB / EBI]
	1F31; X-ray; A=1-1290. [ExPASy / RCSB / EBI]
	1F82; X-ray; A=1-424. [ExPASy / RCSB / EBI]
	1F83; X-ray; A=1-425. [ExPASy / RCSB / EBI]
	1FQH; X-ray; A=1-424. [ExPASy / RCSB / EBI]
	1G9A; X-ray; A=1-1290. [ExPASy / RCSB / EBI]
	1G9B; X-ray; A=1-1290. [ExPASy / RCSB / EBI]
	1G9C; X-ray; A=1-1290. [ExPASy / RCSB / EBI]
	1G9D; X-ray; A=1-1290. [ExPASy / RCSB / EBI]
PDB	1I1E; X-ray; A=1-1290. [ExPASy / RCSB / EBI]
	1S0B; X-ray; A=1-1290. [ExPASy / RCSB / EBI]
	1S0C; X-ray; A=1-1290. [ExPASy / RCSB / EBI]
	1S0D; X-ray; A=1-1290. [ExPASy / RCSB / EBI]
	1S0E; X-ray; A=1-1290. [ExPASy / RCSB / EBI]
	1S0F; X-ray; A=1-1290. [ExPASy / RCSB / EBI]
	1S0G; X-ray; A=1-1290. [ExPASy / RCSB / EBI]
	1Z0H; X-ray; A/B=-. [ExPASy / RCSB / EBI]
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MEROPS	M27.002; -.
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InterPro	IPR006025; Pept_M_Zn_BS.
	IPR000395; Peptidase_M27.
	Graphical view of domain structure.
Pfam	PF01742; Peptidase_M27; 1.
	Pfam graphical view of domain structure.
PRINTS	PR00760; BONTOXILYSIN.
ProDom	PD001963; Botulinum; 1.
	[Domain structure / List of seq. sharing at least 1 domain]
PROSITE	PS00142; ZINC_PROTEASE; 1.
HOGENOM	[Family / Alignment / Tree]
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ProtoNet	P10844.
ProtoMap	P10844.
PRESAGE	P10844.
DIP	P10844.
ModBase	P10844.
SWISS-2DPAGE	Get region on 2D PAGE.
UniRef	View cluster of proteins with at least 50% / 90% identity.
Keywords	

3D-structure; Direct protein sequencing; Hydrolase; Metalloprotease; Neurotoxin; Protease; Toxin; Transmembrane; Zinc.

Features

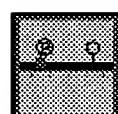


Feature table viewer



Feature aligner

PIR	A48940; A48940.
	1EPW; X-ray; A=1-1290. [ExPASy / RCSB / EBI]
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	1G9B; X-ray; A=1-1290. [ExPASy / RCSB / EBI]
	1G9C; X-ray; A=1-1290. [ExPASy / RCSB / EBI]
	1G9D; X-ray; A=1-1290. [ExPASy / RCSB / EBI]
PDB	1I1E; X-ray; A=1-1290. [ExPASy / RCSB / EBI]
	1S0B; X-ray; A=1-1290. [ExPASy / RCSB / EBI]
	1S0C; X-ray; A=1-1290. [ExPASy / RCSB / EBI]
	1S0D; X-ray; A=1-1290. [ExPASy / RCSB / EBI]
	1S0E; X-ray; A=1-1290. [ExPASy / RCSB / EBI]
	1S0F; X-ray; A=1-1290. [ExPASy / RCSB / EBI]
	1S0G; X-ray; A=1-1290. [ExPASy / RCSB / EBI]
	1Z0H; X-ray; A/B=-. [ExPASy / RCSB / EBI]
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Keywords	3D-structure; Direct protein sequencing; Hydrolase; Metalloprotease; Neurotoxin; Protease; Toxin; Transmembrane; Zinc.

Features

Feature table viewer



Feature aligner

Key	From	To	Length	Description
INIT_MET	0	0		
CHAIN	1	440	440	Botulinum neurotoxin B light-chain.
CHAIN	441	1290	850	Botulinum neurotoxin B heavy-chain.
ACT_SITE	230	230		<i>By similarity.</i>
METAL	229	229		Zinc (catalytic) (<i>By similarity</i>).
METAL	233	233		Zinc (catalytic) (<i>By similarity</i>).
DISULFID	436	445		Interchain (between light and heavy chains) <i>(Probable)</i> .
CONFLICT	29	29		T -> M (in Ref. 4).
CONFLICT	217	217		R -> G (in Ref. 2).
CONFLICT	224	224		A -> S (in Ref. 2).
CONFLICT	463	463		S -> R (in Ref. 4).
TURN	9	10	2	
STRAND	18	22	5	
HELIX	24	26	3	
TURN	27	28	2	
STRAND	33	39	7	
TURN	40	41	2	
STRAND	42	45	4	
TURN	51	52	2	
HELIX	55	58	4	
STRAND	63	64	2	
TURN	67	68	2	
STRAND	71	73	3	
TURN	75	78	4	
HELIX	81	98	18	
TURN	99	100	2	
HELIX	102	113	12	
TURN	121	122	2	
TURN	125	126	2	
STRAND	127	128	2	
TURN	133	135	3	
STRAND	136	140	5	
TURN	144	145	2	
STRAND	150	154	5	
STRAND	157	160	4	
STRAND	165	165	1	
TURN	166	167	2	
STRAND	170	172	3	
STRAND	175	176	2	
TURN	177	178	2	
STRAND	179	180	2	
HELIX	181	183	3	
TURN	184	185	2	
STRAND	190	193	4	
STRAND	198	202	5	
TURN	205	206	2	

Key	From	To	Length	Description
INIT_MET	0	0		
CHAIN	1	440	440	Botulinum neurotoxin B light-chain.
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TURN	9	10	2	
STRAND	18	22	5	
HELIX	24	26	3	
TURN	27	28	2	
STRAND	33	39	7	
TURN	40	41	2	
STRAND	42	45	4	
TURN	51	52	2	
HELIX	55	58	4	
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TURN	67	68	2	
STRAND	71	73	3	
TURN	75	78	4	
HELIX	81	98	18	
TURN	99	100	2	
HELIX	102	113	12	
TURN	121	122	2	
TURN	125	126	2	
STRAND	127	128	2	
TURN	133	135	3	
STRAND	136	140	5	
TURN	144	145	2	
STRAND	150	154	5	
STRAND	157	160	4	
STRAND	165	165	1	
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STRAND	175	176	2	
TURN	177	178	2	
STRAND	179	180	2	
HELIX	181	183	3	
TURN	184	185	2	
STRAND	190	193	4	
STRAND	198	202	5	
TURN	205	206	2	

TURN	210	211	2
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HELIX	223	238	16
TURN	239	240	2
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STRAND	250	250	1
TURN	255	256	2
STRAND	257	257	1
STRAND	263	263	1
HELIX	265	271	7
TURN	273	274	2
HELIX	275	278	4
HELIX	281	304	24
STRAND	307	308	2
TURN	312	313	2
HELIX	316	326	11
TURN	327	328	2
STRAND	330	331	2
TURN	333	334	2
STRAND	337	338	2
HELIX	341	353	13
TURN	354	354	1
HELIX	357	364	8
TURN	365	365	1
STRAND	377	382	6
TURN	385	386	2
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STRAND	392	392	1
TURN	393	395	3
STRAND	396	396	1
TURN	397	397	1
HELIX	400	402	3
TURN	403	403	1
HELIX	406	411	6
STRAND	412	412	1
TURN	413	415	3
HELIX	417	419	3
STRAND	420	421	2
HELIX	425	427	3
STRAND	428	429	2
STRAND	432	436	5
STRAND	445	449	5
HELIX	450	452	3
STRAND	454	454	1
STRAND	457	457	1
HELIX	459	461	3
HELIX	465	467	3
STRAND	470	472	3

TURN	210	211	2
STRAND	219	220	2
HELIX	223	238	16
TURN	239	240	2
STRAND	248	248	1
STRAND	250	250	1
TURN	255	256	2
STRAND	257	257	1
STRAND	263	263	1
HELIX	265	271	7
TURN	273	274	2
HELIX	275	278	4
HELIX	281	304	24
STRAND	307	308	2
TURN	312	313	2
HELIX	316	326	11
TURN	327	328	2
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TURN	333	334	2
STRAND	337	338	2
HELIX	341	353	13
TURN	354	354	1
HELIX	357	364	8
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STRAND	377	382	6
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HELIX	406	411	6
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HELIX	425	427	3
STRAND	428	429	2
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HELIX	787	811	25
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HELIX	859	862	4
STRAND	863	869	7
STRAND	874	876	3

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STRAND	969	975	7
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STRAND	981	987	7
TURN	998	999	2
STRAND	1002	1008	7
STRAND	1012	1017	6
TURN	1018	1019	2
STRAND	1020	1026	7
STRAND	1038	1045	8
TURN	1049	1050	2
STRAND	1053	1061	9
HELIX	1067	1078	12
STRAND	1082	1082	1
STRAND	1084	1084	1
TURN	1086	1087	2
STRAND	1090	1090	1
STRAND	1092	1093	2
TURN	1094	1094	1
STRAND	1096	1101	6
TURN	1102	1103	2
TURN	1105	1106	2
STRAND	1107	1111	5
TURN	1113	1114	2
STRAND	1118	1122	5
STRAND	1125	1125	1
STRAND	1136	1136	1
STRAND	1144	1148	5
STRAND	1158	1159	2
STRAND	1161	1161	1
TURN	1162	1163	2
STRAND	1165	1172	8
TURN	1173	1174	2
STRAND	1175	1182	8

TURN	1183	1184	2
STRAND	1189	1191	3
STRAND	1193	1196	4
TURN	1201	1202	2
STRAND	1203	1204	2
STRAND	1207	1210	4
STRAND	1220	1225	6
STRAND	1233	1245	13
STRAND	1250	1259	10
TURN	1260	1260	1
HELIX	1261	1265	5
TURN	1266	1267	2
TURN	1273	1274	2
TURN	1276	1277	2
STRAND	1279	1282	4
STRAND	1285	1285	1
TURN	1286	1287	2
STRAND	1288	1288	1

Sequence information

Length: 1290 AA [This is the length of the unprocessed precursor]

Molecular weight: 150671 Da
[This is the MW of the unprocessed precursor]

CRC64: D21746E2C024DF43 [This is a checksum on the sequence]

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PVTINNFNYN	DPIDNNNIIM	MEPPFARGTG	RYYKAFKITD	RIWIIPERYT	FGYKPEDFNK
70	80	90	100	110	120
SSGIFNRDVC	EYYDPDYLNT	NDKKNIFLQT	MIKLFNRIKS	KPLGEKLLEM	IINGIPYLGD
130	140	150	160	170	180
RRVPLEEFNT	NIASVTVNKL	ISNPGEVERK	KGIFANLIIF	GPGPVLNENE	TIDIGIQNHF
190	200	210	220	230	240
ASREGFGGIM	QMKFCPEYVS	VFNNVQENKG	ASIFNRRGYF	SDPALILMHE	LIHVLHGLYG
250	260	270	280	290	300
IKVDDLPIVP	NEKKFFMQST	DAIQAEELYT	FGGQDPSIIT	PSTDKSIYDK	VLQNFRGIVD
310	320	330	340	350	360
RLNKVILVCIS	DPNININIYK	NKFKDKYKFKV	EDSEGKYSID	VESFDKLYKS	LMFGFTETNI
370	380	390	400	410	420
AENYKIKTRA	SYFSDSLPpv	KIKNLLDNEI	YTIEEGFNIS	DKDMEKEYRG	QNKAINKQAY
430	440	450	460	470	480
EEISKEHLAV	YKIQMCKSVK	APGICIDVDN	EDLFFIADKN	SFSDDLSKNE	RIEYNTQSNY
490	500	510	520	530	540
IENDFPINEL	ILDSDLISKI	ELPSENTESL	TDFNVDVPVY	EKOQPAIKKIF	TDENTIFQYL
550	560	570	580	590	600
YSQTFPLDIR	DISLTSSFDD	ALLFSNKVYS	FFSMDYIKTA	NKVVEAGLFA	GWVKQIVNDF
610	620	630	640	650	660
VIEANKNSTM	DKIADISLIV	PYIGLALNVG	NETAKGNFEN	AFEIAGASIL	LEFIPELLIP

TURN	1183	1184	2
STRAND	1189	1191	3
STRAND	1193	1196	4
TURN	1201	1202	2
STRAND	1203	1204	2
STRAND	1207	1210	4
STRAND	1220	1225	6
STRAND	1233	1245	13
STRAND	1250	1259	10
TURN	1260	1260	1
HELIX	1261	1265	5
TURN	1266	1267	2
TURN	1273	1274	2
TURN	1276	1277	2
STRAND	1279	1282	4
STRAND	1285	1285	1
TURN	1286	1287	2
STRAND	1288	1288	1

Sequence information

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10	20	30	40	50	60
PVTINNFNYN	DPIDNNNIIM	MEPPFARGTG	RYYKAFKITD	RIWIIPERYT	FGYKPEDFNK
70	80	90	100	110	120
SSGIFNRDVC	EYYDPDYLNT	NDKKNIFLQT	MIKLFNRIKS	KPLGEKLLEM	IINGIPYLGD
130	140	150	160	170	180
RRVPLEEFNT	NIASVTVNKL	ISNPGEVERK	KGIFANLIIF	GPGPVLNENE	TIDIGIQNHF
190	200	210	220	230	240
ASREGFGGIM	QMKFCPEYVS	VFNNVQENKG	ASIFNRRGYF	SDPALILMHE	LIHVLHGLYG
250	260	270	280	290	300
IKVDDLPPIVP	NEKKFFMQST	DAIQAEELYT	FGGQDPSIIT	PSTDKSIYDK	VLQNFRGIVD
310	320	330	340	350	360
RLNKVLCIS	DPNININIYK	NKFKDKYKFW	EDSEGKYSID	VESFDKLYKS	LMFGFTETNI
370	380	390	400	410	420
AENYKIKTRA	SYFSDSLPPV	KIKNLLDNEI	YTIEEGFNIS	DKDMEKEYRG	QNKAINKQAY
430	440	450	460	470	480
EEISKEHLAV	YKIQMCKSVK	APGICIDVDN	EDLFFIADKN	SFSDDLSKNE	RIEYNTQSNSY
490	500	510	520	530	540
IENDFPINEL	ILDSDLISKI	ELPSENTESL	TDFNVDVPVY	EKQPAIKKIF	TDENTIFQYL
550	560	570	580	590	600
YSQTFPLDIR	DISLTSSFDD	ALLFSNKVYS	FFSMDYIKTA	NKVVEAGLFA	GWVKQIVNDF
610	620	630	640	650	660
VIEANKSNTM	DKIADISLIV	PYIGLALNVG	NETAKGNFEN	AFEIAGASIL	LEFIPELLIP

670 680 690 700 710 720
 VVGAFLLESY IDNKNKIIKT IDNALTKRNE KWSDMYGLIV AQWLSTVNTQ FYTIKEGMYK
 730 740 750 760 770 780
 ALNYQAQALE EIIKYRYNIY SEKEKSNNINI DFNDINSKLN EGINQAIDNI NNFINGCSVS
 790 800 810 820 830 840
 YLMKKMIPLA VEKLDFDNT LKKNLLNYID ENKLYLIGSA EYEKSKVNKY LKTIMPFDLS
 850 860 870 880 890 900
 IYTNDTILIE MFNKYNSEIL NNIILNLRYK DNNLIDLDSGY GAKVEVYDGV ELNDKNQFKL
 910 920 930 940 950 960
 TSSANSKIRV TQNQNIIFNS VFLDFSVSFW IRIPKYKNDG IQNYIHNEYT IINCMKNNSG
 970 980 990 1000 1010 1020
 WKISIRGNRI IWTLIDINGK TKSVFFEYNI REDISEYIINR WFFVTITNNL NNAKIYINGK
 1030 1040 1050 1060 1070 1080
 LESNTDIKDI REVIANGEII FKLDGDDIDRT QFIWMKYFSI FNTELSQSNI EERYKIQSYS
 1090 1100 1110 1120 1130 1140
 EYLKDFWGNP LMYNKEYYMF NAGNKNSYIK LKKDSPVGEI LTRSKYNQNS KYINYRDLYI
 1150 1160 1170 1180 1190 1200
 GEKFIIRRKS NSQSINDDIV RKEDYIYLDL FNLNQEWRVY TYKYFKKEEE KLFLAPISDS
 1210 1220 1230 1240 1250 1260
 DEFYNTIQIK EYDEQPTYSC QLLFKKDEES TDEIGLIGIH RFYESGIVFE EYKDYFCISK
 1270 1280 1290
 WYLKEVKRKP YNLKLGNCNWQ FIPKDEGWTE

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Compute pI/Mw, PeptideMass, PeptideCutter,
Dotlet (Java)

 ScanProsite, MotifScan



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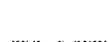
670 680 690 700 710 720
 VVGAFLLESY IDNKNKIIKT IDNALTKRNE KWSDMYGLIV AQWLSTVNTQ FYTIKEGMYK
 730 740 750 760 770 780
 ALNYQAQALE EIIKYRYNIY SEKEKSNNINI DFNDINSKLN EGINQAIIDNI NNFINGCSV
 790 800 810 820 830 840
 YLMKKMIPLA VEKLDFDNT LKKNLLNYID ENKLYLIGSA EYEKS KVNKY LKTIMPFDLS
 850 860 870 880 890 900
 IYTNDTILIE MFNKYNSEIL NNIILNLRYK DNNLIDLGSY GAKVEVYDGV ELNDKNQFKL
 910 920 930 940 950 960
 TSSANSKIRV TQNQNIIFNS VFLDFSVFW IRIPKYKNDG IQNYIHNEYT IINC MKNNSG
 970 980 990 1000 1010 1020
 WKISIRGNRI IWTLIDINGK TKSVFFEYNI REDISEYINR WFFVTITNNL NNAKIYINGK
 1030 1040 1050 1060 1070 1080
 LESNTTDIKDI REVIANGEII FKLDGDDIDRT QFIWMKYFSI FNTELSQSNI EERYKIQSYS
 1090 1100 1110 1120 1130 1140
 EYLKDFWGNP LMYNKEYYMF NAGNKNSYIK LKKDSPVGEI LTRSKYNQNS KYINYRDLYI
 1150 1160 1170 1180 1190 1200
 GEKFIIRRKS NSQSINDDIV RKEDYIYLDL FNLNQEWRVY TYKYFKKEEE KLFLAPISDS
 1210 1220 1230 1240 1250 1260
 DEFYNTIQIK EYDEQPTYSC QLLFKKDEES TDEIGLIGH RFYESGIVFE EYKDYFCISK
 1270 1280 1290
 WYLKEVKRKP YNLKLGNCNWQ FIPKDEGWTE

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In case of problems, please read the [online BLAST help](#).
If your question is not covered, please contact <helpdesk@expasy.org>.

NCBI BLAST program reference [PMID:[9254694](#)]:

Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

Query: 465 AA (of which 5% low-complexity regions filtered out)

Date run: 2005-05-12 15:03:56 UTC+0100 on sib-gml.unil.ch

Program: NCBI BLASTP 1.5.4-Paracel [2003-06-05]

Database: EXPASY/UniProtKB

1,906,987 sequences; 613,355,151 total letters

UniProt Release 5.0 consists of: Swiss-Prot Release 47.0 of 10-May-2005: 181571 entries
TrEMBL Release 30.0 of 10-May-2005: 1714475 entries

Taxonomic view	NiceBlast view	Printable view
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List of potentially matching sequences

Send selected sequences to	Clustal W (multiple alignment)	Submit Query
Select up to		

Include query sequence

Db	AC	Description	Score	E-value
<input type="checkbox"/>	sp_E10844	BXB_CLOBO Botulinum neurotoxin type B precursor (EC 3...	<u>905</u>	0.0
<input type="checkbox"/>	tr_Q93G71	_CLOBO Neurotoxin type B [Clostridium botulinum]	<u>853</u>	0.0
<input type="checkbox"/>	tr_Q933K0	_CLOBO Type B cryptic neurotoxin [Clostridium botulinum]	<u>852</u>	0.0
<input type="checkbox"/>	tr_Q9ZAJ8	_CLOBO BoNT protein [bonT] [Clostridium botulinum]	<u>850</u>	0.0
<input type="checkbox"/>	tr_Q8GR96	_CLOBO Neurotoxin [bontb] [Clostridium botulinum]	<u>831</u>	0.0
<input type="checkbox"/>	tr_Q08077	_CLOBO BoNT/B [bont/b] [Clostridium botulinum]	<u>800</u>	0.0
<input type="checkbox"/>	tr_Q9X708	_CLOBO Botulinum neurotoxin type B (Fragment) [boNT/B] ...	<u>791</u>	0.0
<input type="checkbox"/>	sp_Q60393	BXG_CLOBO Botulinum neurotoxin type G precursor (EC 3...	<u>468</u>	e-130
<input type="checkbox"/>	sp_P10845	BXA1_CLOBO Botulinum neurotoxin type A precursor (EC 3...	<u>316</u>	6e-85
<input type="checkbox"/>	tr_Q7B8V4	_CLOBO BoNT/A [bont/a] [Clostridium botulinum]	<u>316</u>	6e-85

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List of potentially matching sequences

Send selected sequences to

Include query sequence

Db	AC	Description	Score	E-value
<input type="checkbox"/>	sp_F10844	BXB_CLOBO Botulinum neurotoxin type B precursor (EC 3....)	905	0.0
<input type="checkbox"/>	tr_Q93G71	_CLOBO Neurotoxin type B [Clostridium botulinum]	853	0.0
<input type="checkbox"/>	tr_Q933K0	_CLOBO Type B cryptic neurotoxin [Clostridium botulinum]	852	0.0
<input type="checkbox"/>	tr_Q9ZAJ8	_CLOBO BoNT protein [bonT] [Clostridium botulinum]	850	0.0
<input type="checkbox"/>	tr_Q8GR96	_CLOBO Neurotoxin [bontb] [Clostridium botulinum]	831	0.0
<input type="checkbox"/>	tr_Q08077	_CLOBO BoNT/B [bont/b] [Clostridium botulinum]	800	0.0
<input type="checkbox"/>	tr_Q9X708	_CLOBO Botulinum neurotoxin type B (Fragment) [boNT/B] ...	791	0.0
<input type="checkbox"/>	sp_Q60393	BXG_CLOBO Botulinum neurotoxin type G precursor (EC 3....)	458	e-130
<input type="checkbox"/>	sp_P10845	BXA1_CLOBO Botulinum neurotoxin type A precursor (EC 3....)	316	6e-85
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<input type="checkbox"/>	tr	<u>Q45851</u>	_9CLOT	Neurotoxin type F [bont /f]	[Clostridium baratii]	301	2e-80
<input type="checkbox"/>	tr	<u>Q45846</u>	_CLOBO	Botulinum neurotoxin type B (Fragment) [BoNT/B] ...	[Clostridium botulinum]	299	1e-79
<input type="checkbox"/>	tr	<u>Q45848</u>	_CLOBO	Botulinum neurotoxin type B (Fragment) [BoNT/B] ...	[Clostridium botulinum]	298	2e-79
<input type="checkbox"/>	sp	<u>Q45894</u>	BXA2_CLOBO	Botulinum neurotoxin type A precursor (EC 3...)	[Clostridium botulinum]	297	3e-79
<input type="checkbox"/>	tr	<u>Q58GH1</u>	_CLOBO	Type A2 botulinum neurotoxin [Clostridium botulinum]		297	3e-79
<input type="checkbox"/>	tr	<u>Q9ZAJ5</u>	_CLOBO	BonT protein [bonT] [Clostridium botulinum]		281	2e-74
<input type="checkbox"/>	tr	<u>Q57236</u>	_CLOBO	BoNT/F (Neurotoxin type F) [bont/f] [Clostridium botulinum]		281	3e-74
<input type="checkbox"/>	sp	<u>P30996</u>	BXF_CLOBO	Botulinum neurotoxin type F precursor (EC 3...)	[Clostridium botulinum]	278	1e-73
<input type="checkbox"/>	sp	<u>Q00496</u>	BXE_CLOBO	Botulinum neurotoxin type E precursor (EC 3...)	[Clostridium botulinum]	273	4e-72
<input type="checkbox"/>	tr	<u>Q9K395</u>	_CLOBU	Type E botulinum toxin [bont/E] [Clostridium butyricum]		267	3e-70
<input type="checkbox"/>	sp	<u>P30995</u>	BXE_CLOBU	Botulinum neurotoxin type E precursor (EC 3...)	[Clostridium butyricum]	266	7e-70
<input type="checkbox"/>	tr	<u>Q9FAR6</u>	_CLOBU	Type E botulinum toxin [bont/E] [Clostridium butyricum]		266	9e-70
<input type="checkbox"/>	tr	<u>Q8KZM3</u>	_CLOBU	Type E botulinum toxin [bont/E] [Clostridium butyricum]		266	9e-70
<input type="checkbox"/>	sp	<u>P19321</u>	BXD_CLOBO	Botulinum neurotoxin type D precursor (EC 3...)	[Clostridium butyricum]	233	7e-60
<input type="checkbox"/>	tr	<u>Q9QTG7</u>	_CBDP	NTX (Fragment) [ntx] [Clostridium botulinum D bacilli]		231	2e-59
<input type="checkbox"/>	tr	<u>Q5DW55</u>	_CLOBO	Type C botulinaum neurotoxin [bont/C] [Clostridium botulinum]		230	6e-59
<input type="checkbox"/>	tr	<u>Q9LBS7</u>	_CLOBO	Type C botulinaum neurotoxin [bont/C] [Clostridium botulinum]		228	3e-58
<input type="checkbox"/>	tr	<u>Q45849</u>	_CLOBO	Neurotoxin [Clostridium botulinum C]		228	3e-58
<input type="checkbox"/>	tr	<u>Q841S3</u>	_CLOBO	Neurotoxin [Clostridium botulinum]		226	6e-58
<input type="checkbox"/>	sp	<u>P04958</u>	TETX_CLOTE	Tetanus toxin precursor (EC 3.4.24.68) (Tetanus toxin)		211	2e-53
<input type="checkbox"/>	tr	<u>Q9LA13</u>	_CLOTE	Tetanus toxin (Fragment) [Clostridium tetani]		211	4e-53
<input type="checkbox"/>	tr	<u>Q45967</u>	_CLOBO	Neurotoxin consisting of botulinum neurotoxin D ...	[Clostridium botulinum]	206	1e-51
<input type="checkbox"/>	tr	<u>Q9LBR1</u>	_CLOBO	Neurotoxin [Clostridium botulinum]		205	1e-51
<input type="checkbox"/>	tr	<u>Q93N27</u>	_CLOTE	Tetanus toxin (Fragment) [Clostridium tetani]		200	5e-50
<input type="checkbox"/>	sp	<u>P18640</u>	BXC1_CLOBO	Botulinum neurotoxin type C1 precursor (EC 3...)	[Clostridium botulinum]	196	2e-49
<input type="checkbox"/>	tr	<u>Q93HT3</u>	_CLOBO	Type C botulinaum neurotoxin [bont/C] [Clostridium botulinum]		198	2e-49
<input type="checkbox"/>	tr	<u>Q7WUH9</u>	_CLOBO	Botulinum neurotoxin type B (Fragment) [bont/B] ...	[Clostridium botulinum]	148	2e-34
<input type="checkbox"/>	tr	<u>Q7WRW0</u>	_CLOBO	Botulinum neurotoxin type B (Fragment) [bont/B] ...	[Clostridium botulinum]	147	6e-34
<input type="checkbox"/>	tr	<u>Q6Q799</u>	_CLOBO	Non-proteolytic neurotoxin type B (Fragment) [Clostridium botulinum]		146	1e-33
<input type="checkbox"/>	tr	<u>Q79AH9</u>	_CLOBO	Botulinum neurotoxin type F (Fragment) [BoNT/F] ...	[Clostridium botulinum]	142	1e-32
<input type="checkbox"/>	tr	<u>Q45861</u>	_CLOBO	Botulinum neurotoxin type E (Fragment) [BoNT/E] ...	[Clostridium botulinum]	133	7e-30
<input type="checkbox"/>	tr	<u>Q06018</u>	_CLOBO	NTNH protein [NTNH] [Clostridium botulinum]		86	2e-15
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<input type="checkbox"/>	sp	<u>P46082</u>	BXEN_CLOBO	Botulinum neurotoxin type E, nontoxic component		75	4e-12
<input type="checkbox"/>	tr	<u>Q9LBS8</u>	_CLOBO	NTNHA [ntnha] [Clostridium botulinum]		75	4e-12
<input type="checkbox"/>	sp	<u>Q06366</u>	BXEN_CLOBU	Botulinum neurotoxin type E, nontoxic component		74	5e-12
<input type="checkbox"/>	tr	<u>Q9ZAJ9</u>	_CLOBO	Ntnh protein [ntnh] [Clostridium botulinum]		74	5e-12
<input type="checkbox"/>	tr	<u>P71117</u>	_CLOBO	Nontoxic-nonhemagglutinin [nontoxic-nonhemagglutinin]		74	5e-12
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<input type="checkbox"/>	tr	<u>Q69277</u>	_CLOBO	Nontoxic-nonhaemagglutinin [ntnh] [Clostridium botulinum]		74	5e-12
<input type="checkbox"/>	tr	<u>Q33871</u>	_CLOBO	Nontoxic-nonhemagglutinin component [ntnh/B] [Clostridium botulinum]		74	5e-12
<input type="checkbox"/>	tr	<u>Q45893</u>	_CLOBO	NTNH protein [ntnh] [Clostridium botulinum]		74	7e-12
<input type="checkbox"/>	tr	<u>Q9LBR2</u>	_CLOBO	NTNHA [ntnha] [Clostridium botulinum]		74	9e-12
<input type="checkbox"/>	sp	<u>P46081</u>	BXCN_CLOBO	Botulinum neurotoxin type C1, nontoxic component		72	3e-11
<input type="checkbox"/>	tr	<u>Q93HT4</u>	_CLOBO	NTNHA [ntnha] [Clostridium botulinum]		72	3e-11

tr	<u>Q45851</u>	_9CLOT	Neurotoxin type F [bont /f]	[Clostridium baratii]	301	2e-80
tr	<u>Q45846</u>	_CLOBO	Botulinum neurotoxin type B (Fragment)	[BoNT/B] ...	299	1e-79
tr	<u>Q45848</u>	_CLOBO	Botulinum neurotoxin type B (Fragment)	[BoNT/B] ...	298	2e-79
sp	<u>Q45894</u>	BXA2_CLOBO	Botulinum neurotoxin type A precursor (EC 3...	... 297	3e-79	
tr	<u>Q58GH1</u>	_CLOBO	Type A2 botulinum neurotoxin [Clostridium botuli...	297	3e-79	
tr	<u>Q9ZAJ5</u>	_CLOBO	BonT protein [bonT] [Clostridium botulinum]	281	2e-74	
tr	<u>Q57236</u>	_CLOBO	BoNT/F (Neurotoxin type F) [bont/f] [Clostridium...	281	3e-74	
sp	<u>P30996</u>	BXF_CLOBO	Botulinum neurotoxin type F precursor (EC 3....	278	1e-73	
sp	<u>Q00496</u>	BXE_CLOBO	Botulinum neurotoxin type E precursor (EC 3....	273	4e-72	
tr	<u>Q9K395</u>	_CLOBU	Type E botulinum toxin [bont/E] [Clostridium but...	267	3e-70	
sp	<u>P30995</u>	BXE_CLOBU	Botulinum neurotoxin type E precursor (EC 3....	266	7e-70	
tr	<u>Q9FAR6</u>	_CLOBU	Type E botulinum toxin [bont/E] [Clostridium but...	266	9e-70	
tr	<u>Q8KZM3</u>	_CLOBU	Type E botulinum toxin [bont/E] [clostridium but...	266	9e-70	
sp	<u>P19321</u>	BXD_CLOBO	Botulinum neurotoxin type D precursor (EC 3....	233	7e-60	
tr	<u>Q9QTG7</u>	_CBDP NTX (Fragment)	[ntx] [Clostridium botulinum D bac...	231	2e-59	
tr	<u>Q5DW55</u>	_CLOBO	Type C botulinaum neurotoxin [bont/C] [Clostridi...	230	6e-59	
tr	<u>Q9LBS7</u>	_CLOBO	Type C botulinaum neurotoxin [bont/C] [Clostridi...	228	3e-58	
tr	<u>Q45849</u>	_CLOBO	Neurotoxin [Clostridium botulinum C]	228	3e-58	
tr	<u>Q841S3</u>	_CLOBO	Neurotoxin [Clostridium botulinum]	226	6e-58	
sp	<u>P04958</u>	TETX_CLOTE	Tetanus toxin precursor (EC 3.4.24.68) (Ten...	211	2e-53	
tr	<u>Q9LA13</u>	_CLOTE	Tetanus toxin (Fragment) [Clostridium tetani]	211	4e-53	
tr	<u>Q45967</u>	_CLOBO	Neurotoxin consisting of botulinum neurotoxin D ...	206	1e-51	
tr	<u>Q9LBR1</u>	_CLOBO	Neurotoxin [Clostridium botulinum]	205	1e-51	
tr	<u>Q93N27</u>	_CLOTE	Tetanus toxin (Fragment) [Clostridium tetani]	200	5e-50	
sp	<u>P18640</u>	BXC1_CLOBO	Botulinum neurotoxin type C1 precursor (EC ...	198	2e-49	
tr	<u>Q93HT3</u>	_CLOBO	Type C botulinaum neurotoxin [bont/C] [Clostridi...	198	2e-49	
tr	<u>Q7WUH9</u>	_CLOBO	Botulinum neurotoxin type B (Fragment) [bont/B] ...	148	2e-34	
tr	<u>Q7WRW0</u>	_CLOBO	Botulinum neurotoxin type B (Fragment) [bont/B] ...	147	6e-34	
tr	<u>Q6Q799</u>	_CLOBO	Non-proteolytic neurotoxin type B (Fragment) [Cl...	146	1e-33	
tr	<u>Q79AH9</u>	_CLOBO	Botulinum neurotoxin type F (Fragment) [BoNT/F] ...	142	1e-32	
tr	<u>Q45861</u>	_CLOBO	Botulinum neurotoxin type E (Fragment) [BoNT/E] ...	133	7e-30	
tr	<u>Q06018</u>	_CLOBO	NTNH protein [NTNH] [Clostridium botulinum]	36	2e-15	
tr	<u>Q45888</u>	_CLOBO	Nontoxic-hemagglutinin [nontoxic-hemagglutinin] ...	77	6e-13	
sp	<u>P46082</u>	BXEN_CLOBO	Botulinum neurotoxin type E, nontoxic compo...	75	4e-12	
tr	<u>Q9LBS8</u>	_CLOBO	NTNHA [ntnha] [Clostridium botulinum]	75	4e-12	
sp	<u>Q06366</u>	BXEN_CLOBU	Botulinum neurotoxin type E, nontoxic compo...	74	5e-12	
tr	<u>Q9ZAJ9</u>	_CLOBO	Ntnh protein [ntnh] [Clostridium botulinum]	74	5e-12	
tr	<u>P71117</u>	_CLOBO	Nontoxic-nonhemagglutinin [nontoxic-nonhemagglut...	74	5e-12	
tr	<u>Q87710</u>	_9CLOT	NTNH protein [ntnh] [Clostridium baratii]	74	5e-12	
tr	<u>Q69277</u>	_CLOBO	Nontoxic-nonhaemagglutinin [ntnh] [Clostridium b...	74	5e-12	
tr	<u>Q33871</u>	_CLOBO	Nontoxic-nonhemagglutinin component [ntnh/B] [Cl...	74	5e-12	
tr	<u>Q45893</u>	_CLOBO	NTNH protein [ntnh] [Clostridium botulinum]	74	7e-12	
tr	<u>Q9LBR2</u>	_CLOBO	NTNHA [ntnha] [Clostridium botulinum]	74	9e-12	
sp	<u>P46081</u>	BXCN_CLOBO	Botulinum neurotoxin type C1, nontoxic comp...	72	3e-11	
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<input type="checkbox"/>	tr Q45916	CLOBO 138kDa protein associated with BoNT /C1-haemaggl...	72	3e-11
<input type="checkbox"/>	tr Q9ZX77	CBDP NTNH [ntnh] [Clostridium botulinum D bacteriophage]	72	3e-11
<input type="checkbox"/>	tr Q38197	9VIRU ANTP-139 protein [ANTP-139] [Clostridium botulin...	72	3e-11
<input type="checkbox"/>	tr Q53550	CLOBO Progenitor toxin L nontoxic-nonhemagglutinin com...	72	3e-11
<input type="checkbox"/>	tr Q45891	CLOBO NTNH protein [ntnh] [Clostridium botulinum]	71	6e-11
<input type="checkbox"/>	tr Q45880	CLOBO NtnhA protein [ntnhA] [Clostridium botulinum]	69	2e-10
<input type="checkbox"/>	tr O69276	CLOBO Nontoxic-nonhaemagglutinin [ntnh] [Clostridium b...	69	2e-10
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<input type="checkbox"/>	tr Q6DN58	KLULA COX1 intron 3 ORF [COX1] [Kluyveromyces lactis (...)	45	0.004
<input type="checkbox"/>	tr Q8I5X3	PLAF7 Hypothetical protein [PFL0360c] [Plasmodium falc...	44	0.008
<input type="checkbox"/>	tr Q7RP92	PLAYO Clp [PY01567] [Plasmodium yoelii yoelii]	44	0.010
<input type="checkbox"/>	tr Q7RDL0	PLAYO Hypothetical protein [PY05412] [Plasmodium yoeli...	44	0.010
<input type="checkbox"/>	tr Q6LFF0	PLAF7 Hypothetical protein [PFF0575c] [Plasmodium falc...	44	0.010
<input type="checkbox"/>	tr Q8IDG1	PLAF7 Hypothetical protein PF13_0283 [PF13_0283] [Plas...	43	0.013
<input type="checkbox"/>	tr Q8I3X5	PLAF7 Hypothetical protein PFE0655w [PFE0655w] [Plasmo...	43	0.013
<input type="checkbox"/>	tr Q7RJM7	PLAYO Hypothetical protein [PY03232] [Plasmodium yoeli...	43	0.013
<input type="checkbox"/>	tr Q9EMF0	AMEPV AMV256 [AMV256] [Amsacta moorei entomopoxvirus (...)	42	0.022
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<input type="checkbox"/>	tr Q7RB20	PLAYO Hypothetical protein [PY06328] [Plasmodium yoeli...	42	0.029
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<input type="checkbox"/>	sp Q98PH2	MTLD_MYCPU Mannitol-1-phosphate 5-dehydrogenase (EC 1....	39	0.19
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<input type="checkbox"/>	tr Q45850	CLOBO Ntnh protein [ntnh] [Clostridium botulinum]	63	2e-08
<input type="checkbox"/>	tr P71108	CLOBO Nontoxic-nonhemagglutinin component [Clostridium...	62	3e-08
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<input type="checkbox"/>	tr Q7WRP2	CLOBU Botulinum neurotoxin type E (Fragment) [bont/E] ...	45	0.003
<input type="checkbox"/>	tr Q6DN58	KLULA COX1 intron 3 ORF [COX1] [Kluyveromyces lactis (...)	45	0.004
<input type="checkbox"/>	tr Q8I5X3	PLAF7 Hypothetical protein [PFL0360c] [Plasmodium falc...	44	0.008
<input type="checkbox"/>	tr Q7RP92	PLAYO Clp [PY01567] [Plasmodium yoelii yoelii]	44	0.010
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<input type="checkbox"/>	tr Q8IDG1	PLAF7 Hypothetical protein PF13_0283 [PF13_0283] [Plas...	43	0.013
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<input type="checkbox"/>	sp P21358	RMAR_CANGA Mitochondrial ribosomal protein VAR1 [VAR1]...	40	0.11
<input type="checkbox"/>	tr Q8II48	PLAF7 Hypothetical protein [PF11_0326] [Plasmodium fal...	40	0.11
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<input type="checkbox"/>	sp Q98PH2	MTLD_MYCPU Mannitol-1-phosphate 5-dehydrogenase (EC 1....	39	0.19
<input type="checkbox"/>	tr Q8ID18	PLAF7 Hypothetical protein MAL13P1.349 [MAL13P1.349] [...]	39	0.19

Graphical overview of the alignments

Click here to resubmit your query after masking regions matching PROSITE profiles or Pfam HMMs
( [Help](#)) (use [ScanProsite](#) for more details about PROSITE matches)

Profile hits 

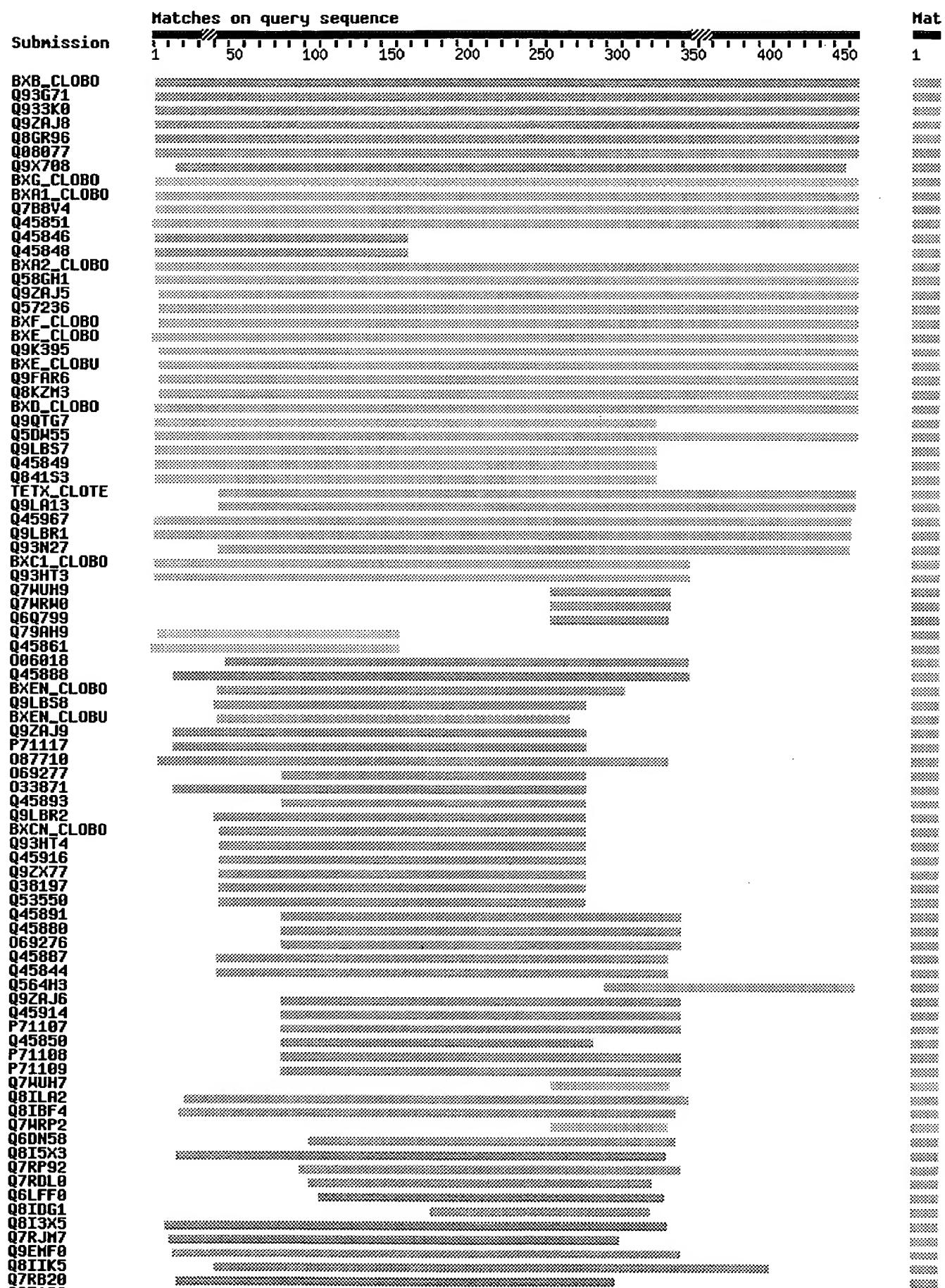
Pfam hits 
Toxin_R_bind_N Toxin_R_bind_C

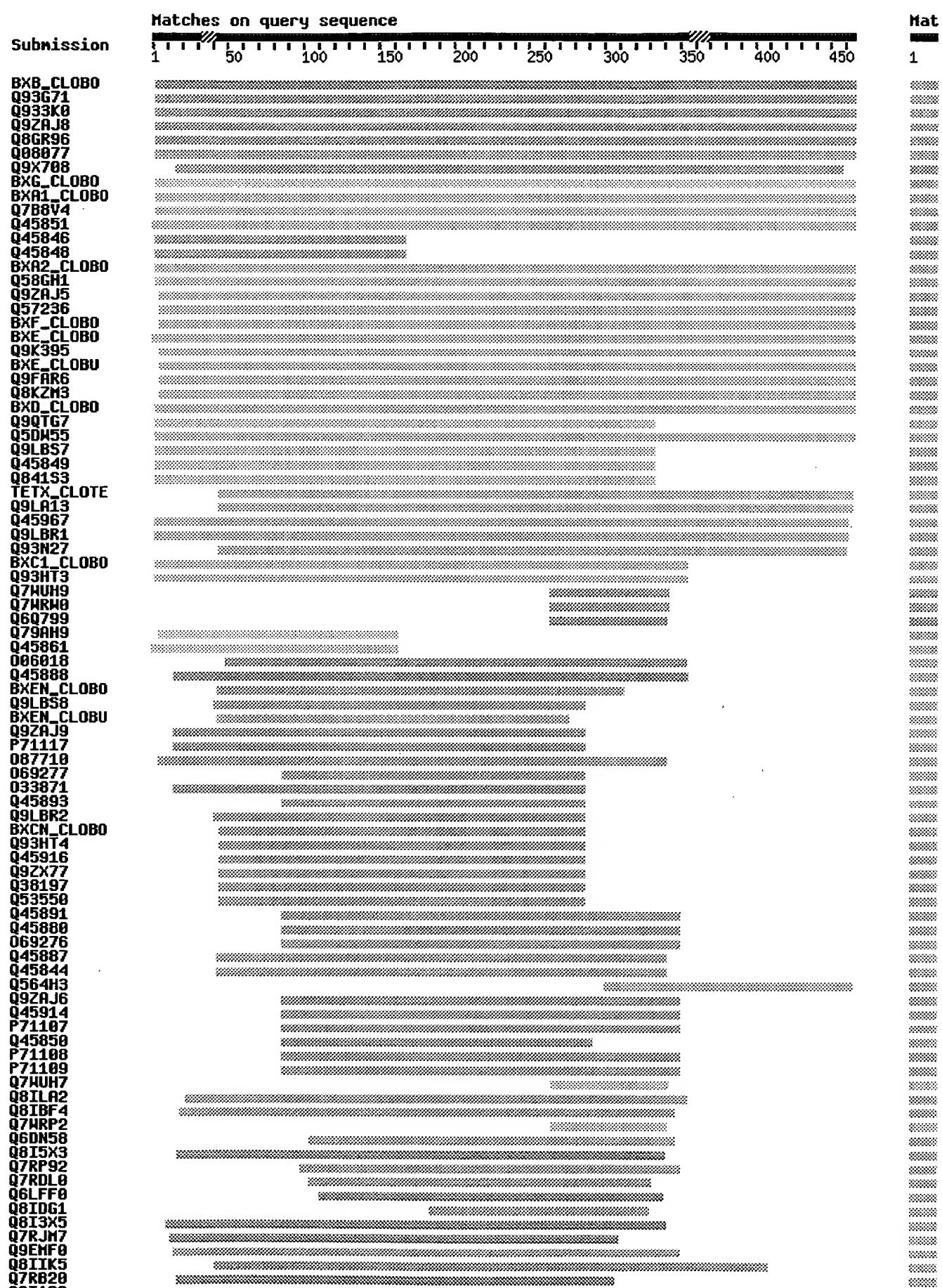
Graphical overview of the alignments

Click here to resubmit your query after masking regions matching PROSITE profiles or Pfam HMMs
( [Help](#)) (use [ScanProsite](#) for more details about PROSITE matches)

Profile hits 

Pfam hits 





Alignments

sp P10844 Botulinum neurotoxin type B precursor (EC 3.4.24.69) 1290
 BXB_CLOBO (BoNT/B) AA
 (Bontoxilysin B) [botB] [Clostridium botulinum] align

Score = 905 bits (2339), Expect = 0.0
 Identities = 441/463 (95%), Positives = 441/463 (95%)

Query: 3 NKYLKTIMPFDSL IYTNDTILIE MFNKYNSE XXXXXXXXRYKDNNLIDLSGYGAKVEVY 62
 NKYLKTIMPFDSL IYTNDTILIE MFNKYNSE RYKDNNLIDLSGYGAKVEVY
 Sbjct: 828 NKYLKTIMPFDSL IYTNDTILIE MFNKYNSE ILLNRLYKDNNLIDLSGYGAKVEVY 887

Query: 63 DGVELNDKNQFKLTSSANSKIRVTQNQNI IFNSVFLDFSVS FWIRIPKYKNDGIQNYIHN 122
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Query: 123 EYTIINCMKNNSGWKISIRGNRI IWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTIT 182
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 Sbjct: 948 EYTIINCMKNNSGWKISIRGNRI IWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTIT 1007

Query: 183 NNLNNNAKIYINGKLESNTDIKDIREVIANGEII FKLDGDIDRTQFIWMKYFSIFNTELSQ 242
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 SNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKN SYIKLKKDSPVGEILTRSKYN
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Query: 303 QNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYI YLDF FNLNQEW RVYXXXXXX 362
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tr Q93G71 Neurotoxin type B [Clostridium botulinum] 1291 AA
 Q93G71_CLOBO align

Score = 853 bits (2204), Expect = 0.0
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 +KYLKT +PFDSL YTN+TILIE+FNKYNSE RY+DN LIDLSGYGAKVEVY
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Query: 63 DGVELNDKNQFKLTSSANSKIRVTQNQNI IFNSVFLDFSVS FWIRIPKYKNDGIQNYIHN 122
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 Sbjct: 889 DGVKLNDKNQFKLTSSANSKIRVIQNQNI IFNSMFLDFSVS FWIRIPKYKNDGIQNYIHN 948

Alignments

sp P10844 Botulinum neurotoxin type B precursor (EC 3.4.24.69) 1290
 BXB_CLOBO (BoNT/B) AA
 (Bontoxilysin B) [botB] [Clostridium botulinum] align

Score = 905 bits (2339), Expect = 0.0
 Identities = 441/463 (95%), Positives = 441/463 (95%)

Query: 3 NKYLKTIMPFDSL IYTNDTILIE MFNKYNSE XXXXXXXXRYKDNNLIDL SGYGAKVEVY 62
 NKYLKTIMPFDSL IYTNDTILIE MFNKYNSE RYKDNNLIDL SGYGAKVEVY
 Sbjct: 828 NKYLKTIMPFDSL IYTNDTILIE MFNKYNSE I LNNI ILNL RYKDNNLIDL SGYGAKVEVY 887

Query: 63 DGVELNDKNQFKLTSSANSKIRVTQNQNI IFNSVFLDFSVSFWIRIPKYKNDGIQNYIHN 122
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Query: 123 EYTIINCMKNNSGWKISIRGNRIIWTLIDINGKT KSVFFEYNIREDISEYINRWF FVTIT 182
 EYTIINCMKNNSGWKISIRGNRIIWTLIDINGKT KSVFFEYNIREDISEYINRWF FVTIT
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Query: 183 NNLNNAKIYINGKLESNTDIKDIREVIANGEII FKLDGDIDRTQF IWMKYFSIFNTELSQ 242
 NNLNNAKIYINGKLESNTDIKDIREVIANGEII FKLDGDIDRTQF IWMKYFSIFNTELSQ
 Sbjct: 1008 NNLNNAKIYINGKLESNTDIKDIREVIANGEII FKLDGDIDRTQF IWMKYFSIFNTELSQ 1067

Query: 243 SNIEERYKIQS YSEYLKDFWG NPLM YNKEYYMF NAGN KNSYIKL KKDS PVGEILTRSKYN 302
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Query: 303 QNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEW RVYXXXXXX 362
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 Sbjct: 1128 QNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEW RVYTYKYF KK 1187

Query: 363 XXXXXXAPISDSDEFYNTIQIKEYDEQPTYSCQLL FKKDEESTDEIGLIGIHRF YESGI 422
 APISDSDEFYNTIQIKEYDEQPTYSCQLL FKKDEESTDEIGLIGIHRF YESGI
 Sbjct: 1188 EEEKLFLAPISDSDEFYNTIQIKEYDEQPTYSCQLL FKKDEESTDEIGLIGIHRF YESGI 1247

Query: 423 VFEEYKDYFCISKWYLKEVKRKP YNLKLG C N WQFIPK D E G W T E 465
 VFEEYKDYFCISKWYLKEVKRKP YNLKLG C N WQFIPK D E G W T E
 Sbjct: 1248 VFEEYKDYFCISKWYLKEVKRKP YNLKLG C N WQFIPK D E G W T E 1290

tr Q93G71 Neurotoxin type B [Clostridium botulinum] 1291 AA
Q93G71_CLOBO align

Score = 853 bits (2204), Expect = 0.0
 Identities = 414/463 (89%), Positives = 429/463 (92%)

Query: 3 NKYLKTIMPFDSL IYTNDTILIE MFNKYNSE XXXXXXXXRYKDNNLIDL SGYGAKVEVY 62
 +KYLKT +PFDSL YTN+TILIE+FNKYN+ RY+DN LIDL SGYGAKVEVY
 Sbjct: 829 DKYLKTSIPFDLSTY TNNTILIEIFNKYNSDILNNI ILNL RYRDNLKLI DLSGYGAKVEVY 888

Query: 63 DGVELNDKNQFKLTSSANSKIRVTQNQNI IFNSVFLDFSVSFWIRIPKYKNDGIQNYIHN 122
 DGVLNDKNQFKLTSSANSKIRVQNQNI IFNS+FLDFSVSFWIRIPKYKNDGIQNYIHN
 Sbjct: 889 DGVKLNDKNQFKLTSSANSKIRVIQNQNI IFNSMFLDFSVSFWIRIPKYKNDGIQNYIHN 948

Query: 123 EYTIINCMKNNSGKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTIT 182
 EYTIINCMKNNSGKISIRGN IIWTLIDINGK KSVFFEY+I+EDISEYINRWFFVTIT
 Sbjct: 949 EYTIINCMKNNSGKISIRGNMIIWTLIDINGKIKSVFFEYSIKEDESEYINRWFFVTIT 1008

Query: 183 NNLNNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQ 242
 NN +NAKIYINGKLES+ DI+DIREVIAN EIIFKLDG+IDRTQFIWMKYFSIFNTELSQ
 Sbjct: 1009 NNSDNNAKIYINGKLESHIDIRDIREVIANDEIIFKLDGNIDRTQFIWMKYFSIFNTELSQ 1068

Query: 243 SNIEERYKIQSYSEYLKDFWGPNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYN 302
 SNIEE YKIQSYSEYLKDFWGPNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYN
 Sbjct: 1069 SNIEEYKIQSYSEYLKDFWGPNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYN 1128

Query: 303 QNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRYXXXXXX 362
 QNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRY
 Sbjct: 1129 QNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRYIYKYFKK 1188

Query: 363 XXXXXXAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGI 422
 APISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGI
 Sbjct: 1189 EEEKLFLAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGI 1248

Query: 423 VFEEYKDYFCISKWLKEVKRKPYNLKGNCNWQFIPKDEGWTE 465
 VF+EYKDYFCISKWLKEVKRKPYN KGNCNWQFIPKDEGWTE
 Sbjct: 1249 VFKEYKDYFCISKWLKEVKRKPYN SKLGNCNWQFIPKDEGWTE 1291

tr	<u>Q933K0</u>	Type B cryptic neurotoxin [Clostridium	1291 AA
	Q933K0_CLOBO	botulinum]	<u>align</u>

Score = 852 bits (2202), Expect = 0.0
 Identities = 414/463 (89%), Positives = 429/463 (92%)

Query: 3 NKYLKTIMPFDSLTYTNDTILIEFMNKYNSEXXXXXXXXXRYKDNNNLIDLGYGAKVEVY 62
 +KYLKT +PFDSL YTN+TILIE+FNKYN+ RY+DN LIDLGYGAKVEVY
 Sbjct: 829 DKYLKTSIPFDLSTYTNNTILIEIFNKYNSDILNNIILNLRYRDNKLIDLGYGAKVEVY 888

Query: 63 DGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVFWIRIPKYKNDGIQNYIHN 122
 DGV+LNQFKLTSSANSKIRVTQNQNIIFNS+FDFSVFWIRIPKYKNDGIQNYIHN
 Sbjct: 889 DGVKLNDKNQFKLTSSANSKIRVTQNQNIIFNSMFLDFSVFWIRIPKYKNDGIQNYIHN 948

Query: 123 EYTIINCMKNNSGKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTIT 182
 EYTIINCMKNNSGKISIRGN IIWTLIDINGK KSVFFEY+I+EDISEYINRWFFVTIT
 Sbjct: 949 EYTIINCMKNNSGKISIRGNMIIWTLIDINGKIKSVFFEYSIKEDESEYINRWFFVTIT 1008

Query: 183 NNLNNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQ 242
 NN +NAKIYINGKLES+ DI+DIREVIAN EIIFKLDG+IDRTQFIWMKYFSIFNTELSQ
 Sbjct: 1009 NNSDNNAKIYINGKLESHIDIRDIREVIANDEIIFKLDGNIDRTQFIWMKYFSIFNTELSQ 1068

Query: 243 SNIEERYKIQSYSEYLKDFWGPNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYN 302
 SNIEE YKIQSYSEYLKDFWGPNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYN
 Sbjct: 1069 SNIEEYKIQSYSEYLKDFWGPNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYN 1128

Query: 303 QNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRYXXXXXX 362
 QNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRY
 Sbjct: 1129 QNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRYIYKYFKK 1188

Query: 123 EYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTIT 182
 EYTIINCMKNNSGWKISIRGN IIWTLIDINGK KSVFFEY+I+EDISEYINRWFFVTIT
 Sbjct: 949 EYTIINCMKNNSGWKISIRGNMIIWTLIDINGKIKSVFFEYSIKEDISEYINRWFFVTIT 1008

Query: 183 NNLNNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGIDIRTQFIWMKYFSIFNTELSQ 242
 NN +NAKIYINGKLES+ DI+DIREVIAN EIIFKLDG+IDRTQFIWMKYFSIFNTELSQ
 Sbjct: 1009 NNSDNNAKIYINGKLESHIDIRDIREVIANDEIIFKLDGNIDRTQFIWMKYFSIFNTELSQ 1068

Query: 243 SNIEERYKIQSSEYLKDFWGPNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYN 302
 SNIEE YKIQSSEYLKDFWGPNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYN
 Sbjct: 1069 SNIEEIYKIQSSEYLKDFWGPNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYN 1128

Query: 303 QNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYXXXXXX 362
 QNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVY
 Sbjct: 1129 QNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYIYKYFKK 1188

Query: 363 XXXXXXAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGI 422
 APISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGI
 Sbjct: 1189 EEEKLFLAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGI 1248

Query: 423 VFEEYKDYFCISKWYLKEVKRKPYNLKGNCNWQFIPKDEGWTE 465
 VF+EYKDYFCISKWYLKEVKRKPYN KGNCNWQFIPKDEGWTE
 Sbjct: 1249 VFKEYKDYFCISKWYLKEVKRKPYN SKLGCNCNWQFIPKDEGWTE 1291

tr	<u>Q933K0</u>	Type B cryptic neurotoxin [Clostridium	1291 AA
	Q933K0_CLOBO	botulinum]	align

Score = 852 bits (2202), Expect = 0.0
 Identities = 414/463 (89%), Positives = 429/463 (92%)

Query: 3 NKYLKTIMPFDLSIYTNDTILIEFMNKNSEXXXXXXXXXRYKDNNLIDLSSGYGAKVEVY 62
 +NKYLKT +PFDSL YTN+TILIE+FNKYNS+ RY+UN LIDLSSGYGAKVEVY
 Sbjct: 829 DKYLKTSIPFDLSTYTNNTILIEIFNKYNSDILNNIILNLRYRDNKLIDLSSGYGAKVEVY 888

Query: 63 DGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVFWIRIPKYKNDGQNYIHN 122
 DGV+LNQKNQFKLTSSANSKIRVTQNQNIIFNS+FLLDFSVFWIRIPKYKNDGQNYIHN
 Sbjct: 889 DGVKLNDKNQFKLTSSANSKIRVTQNQNIIFNSMFLDFSVFWIRIPKYKNDGQNYIHN 948

Query: 123 EYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTIT 182
 EYTIINCMKNNSGWKISIRGN IIWTLIDINGK KSVFFEY+I+EDISEYINRWFFVTIT
 Sbjct: 949 EYTIINCMKNNSGWKISIRGNMIIWTLIDINGKIKSVFFEYSIKEDISEYINRWFFVTIT 1008

Query: 183 NNLNNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGIDIRTQFIWMKYFSIFNTELSQ 242
 NN +NAKIYINGKLES+ DI+DIREVIAN EIIFKLDG+IDRTQFIWMKYFSIFNTELSQ
 Sbjct: 1009 NNSDNNAKIYINGKLESHIDIRDIREVIANDEIIFKLDGNIDRTQFIWMKYFSIFNTELSQ 1068

Query: 243 SNIEERYKIQSSEYLKDFWGPNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYN 302
 SNIEE YKIQSSEYLKDFWGPNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYN
 Sbjct: 1069 SNIEEIYKIQSSEYLKDFWGPNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYN 1128

Query: 303 QNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYXXXXXX 362
 QNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVY
 Sbjct: 1129 QNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYIYKYFKK 1188

Query: 363 XXXXXXXAPISDSDEFYNTIQIKEKEYDEQPTYSQLLFKKDEESTDEIGLIGHRFYESGI 422
 APISDSDEFYNTIQIKEKEYDEQPTYSQLLFKKDEESTDEIGLIGHRFYESGI
Sbjct: 1189 EEEKLFLAPISDSDEFYNTIQIKEKEYDEQPTYSQLLFKKDEESTDEIGLIGHRFYESGI 1248

Query: 423 VFEEYKDYFCISKWYLKEVKRKPYNLKGNCNWQFIPKDEGWTE 465
 VF+EYKDYFCISKWYLKEVKRKPYNLKGNCNWQFIPKDEGWTE
Sbjct: 1249 VFKEYKDYFCISKWYLKEVKRKPYNNSKLGNCNWQFIPKDEGWTE 1291

tr Q9ZAJ8 BonT protein [bonT] [Clostridium
Q9ZAJ8_CLOBO botulinum] 1291 AA
align

Score = 850 bits (2196), Expect = 0.0
Identities = 413/463 (89%), Positives = 428/463 (92%)

Query: 3 NKYLKTIIMPFDLSIYTNTDILIEFMNKYNSEXXXXXXXXXRYKDNNLIDLSGYGAKVEVY 62
+KYLT +PFDLIS YTN+TILIE+FMKYNSE+ KY+DN LIDLSGYGAKVEVY
Sbjct: 829 DKYLKTSIPFDLSTYTNNTILIEFMNKYNSDILNNIILNLRDNKLIDLSGYGAKVEVY 888

Query: 63 DGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVFWIRIPKYKNDGIONYIHN 122
DGV+LNDKNQFKLTSSANSKIRVQNQNTFNS+FLDFSVFWIRIPKYKNDGIONYIHN
Sbjct: 889 DGVKLNDKNQFKLTSSANSKIRVIONONIIFNSMFLDFSVFWIRIPKYKNDGIONYIHN 948

Query: 123 EYTIINCMKNNSGWKISIRGNRIWTLIDINGKTSVFFEYNIREDISEYINRWFVTIT 182
EYTIINCMKNNSGWKISIRGN RIWTLIDINGK KSVFFEY+I+EDISEYINRWFVTIT
Sbjct: 949 EYTIINCMKNNSGWKISIRGNMIWTLIDINGKIKSVFFEYSIKEDESEYINRWFVTIT 1008

Query: 183 NNLLNNAKIYINGKLESNTDIKDIREVIANGEIIIFKLGDGIDRTQFIWMKYFSIFNTELSQ 242
NN +NAKIYINGKLES+ DT+DIREVIAN EIIIFKLGD+IDRTQFIWMKYFSIFNTELSQ
Sbjct: 1009 NSNDNAKIYINGKLESHIDIRDIREVIANDEIIIFKLGNIDRTQFIWMKYFSIFNTELSQ 1068

Query: 243 SNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKN SYIKLKKD SPVGEILTRSKYN 302
Sbjct: 1069 SNIEE YKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKN SYIKLKKD S VGEILTRSKYN 1128

Query: 303 QNSKYINYRDLYIGEKFIIIRRKSNSQLSINDDIVRKEDYIYLDFNLFNLNQEWRVYXXXXXX 362
QNSKYINYRDLYIGEKFIIIRRKSNSQLSINDDIVRKEDYIYLDFNLFNLNQEWRVY
Sbjct: 1129 QNSKYINYRDLYIGEKFIIIRRKSNSQLSINDDIVRKEDYIYLDFNLFNLNQEWRVYMYKFKK 1188

Query: 363 XXXXXXXXAPISDSDEFYNTIQIKEYDEQPTYSQCQLLFKKDEESTDEIGLIGIHRFYESGI 422

Sbjct: 1189 EEEKLFLAPISDSDEFYNTIQIKEYDEQPTYSQQLFFKKDEESTDEIGLIGHRFYEGI 1248

Query: 423 VFEEYKDYFCISKWYLKEVKRKPYNLKLGCNQWFIPKDEGWTE 465

V F + E Y K D Y F C I S K W Y L K E V R R K P Y N K L G C N W Q F I P K D B G W T E

tr Q8GR96 Neurotoxin [bontb] [Clostridium botulinum] 1291 AA
Q8GR96_CLOBO align

Score = 831 bits (2146), Expect = 0.0
Identities = 403/463 (87%), Positives = 423/463 (91%)

Query: 3 NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXRYKDNNLIDLSGYGAKEVY 62

Query: 363 XXXXXXXAPISDSDEFYNTIQIKEKEYDEQPTYSQLLFKKDEESTDEIGLIGHRFYESGI 422
 APISDSDEFYNTIQIKEKEYDEQPTYSQLLFKKDEESTDEIGLIGHRFYESGT
Sbjct: 1189 EEEKLFLAPISDSDEFYNTIQIKEKEYDEQPTYSQLLFKKDEESTDEIGLIGHRFYESGI 1248

Query: 423 VFEEYKDYFCISKWYLKEVKRKPYNLKGNCNWQFIPKDEGWTE 465
 VF+EYKDYFCISKWYLKEVKRKPYNLKGNCNWQFIPKDEGWTE
Sbjct: 1249 VFKEYKDYFCISKWYLKEVKRKPYNNSKLGNCNWQFIPKDEGWTE 1291

tr Q9ZAJ8 BonT protein [bonT] [Clostridium
Q9ZAJ8_CLOBO botulinum] 1291 AA
align

Score = 850 bits (2196), Expect = 0.0
Identities = 413/463 (89%), Positives = 428/463 (92%)

Query: 3 NKYLKTIIMPFDLSIYTNTDILIEFMFNKYNSXXXXXXXXXRYKDNNNLIDLSGYGAKVEVY 62
+KYLT +PFDSL YTN+TILIE+FMKYNS+ KY+DN LIDLSGYGAKVEVY
Sbjct: 829 DKYLKTSIPFDLSTYTNNTILIEIFNKYNSDILNNIILNLRYRDNKLIDLSGYGAKVEVY 888

Query: 63 DGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHN 122
DGV+LNDKNQFKLTSSANSKIRVQNQNIIFNS+FLDFSVSFWIRIPKYKNDGIQNYIHN
Sbjct: 889 DGVKLNDKNQFKLTSSANSKIRVIONONIIFNSMFLDFSVSFWIRIPKYKNDGIQNYIHN 948

Query: 123 EYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTSVFFEYNIREDISEYINRWFVTIT 182
EYTIINCMKNNSGWKISIRGN IIWTLIDINGK KSVFFEY+I+EDISEYINRWFVTIT
Sbjct: 949 EYTIINCMKNNSGWKISIRGNMIWTLIDINGKIKSVFFEYSIKEDISEYINRWFVTIT 1008

Query: 183 NNLLNNAKIYINGKLESNTDIKDIREVIANGEIIIFKLDGDIDRTQFIWMKYFSIFNTESLQ 242
RN +NAKIYINGKLES+ DT+DIREVIAN BIIIFKLEG+IDRTQFIWMKYFSIFNTESLQ
Sbjct: 1009 NNSDNAKIYINGKLESHIDIRDIREVIANDEIIIFKLDGNIDRTQFIWMKYFSIFNTESLQ 1068

Query: 243 SNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFAGNKNSYIKLKKDS PVGEILTRSKYN 302
 SNIEEE YKIQSYSEYLKDFWGNPLMYNKEYYMFAGNKNSYIKLKKDS VGEILTRSKYN
Sbjct: 1069 SNIEEIYKIQSYSEYLKDFWGNPLMYNKEYYMFAGNKNSYIKLKKDSVGEILTRSKYN 1128

Query: 363 XXXXXXXAPISDSDEFYNTIQIKEKEYDEQPTYSQLLFKKDEESTDEIGLIGIHRFYESGI 422
 APISDSDEFYNTIQIKEKEYDEQPTYSQLLFKKDEESTDEIGLIGIHRFYESGI
Sbjct: 1189 EEEKLELAPISDSDEFYNTIQIKEKEYDEQPTYSQLLFKKDEESTDEIGLIGIHRFYESGI 1248

ISSN: 1169-226X • 15355 • 114 • 12-13

Query: 423 VFELTKDIFCISKWYLKEVAKRPFINERKGNCNWQFIPKDEGWTE 485
VF+EYKDYFCISWKYLKEVKRKPYN KLGCNWQFIPKDEGWTE
Sbjct: 1249 VFKEYKDYFCISKWYLKEVKRKPYN SKLGNCNWQFIPKDEGWTE 1291

Score = 831 bits (2146), Expect = 0.0
Identities = 403/463 (87%), Positives = 423/463 (91%)

Query: 3 NKYLKTIMPFDSLITYNTDTILIEMFNKYNSEXXXXXXXXXRYKDNNLIDLSGYGA
KVEVY 62

Sbjct: 829	+K+LKTII+PFDSL+S+YTN+TILIE+FNKYNS DKHLKTIIPFDLSMYTNNTILIEIFNKYNSEILNNIILNLRYRDNNLIDLSGYGANVEVY	RY+UNNLLIDLSGYGA VEVY 888
Query: 63	DGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVFWIRIPKYKNDGIQNYIHN DGVELNDKNQFKLTSS NS+IRVTQNQNIIFNSVFLDFSVFWIRIPKYKNDGIQNYIHN	122
Sbjct: 889	DGVELNDKNQFKLTSSTNSEIRVTQNQNIIFNSMFLDFSVFWIRIPKYKNDGIQNYIHN	948
Query: 123	EYTIINCCKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTIT EYTIINCCKNNSGWKISIRGNRIIWTL DINGKTKSVFFEY+IREDIS+YINRWFFVTIT	182
Sbjct: 949	EYTIINCCKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYSIREDISDYINRWFFVTIT	1008
Query: 183	NNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTESQ NN +NAKIYINGKLESN DIKDI EVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTESQ	242
Sbjct: 1009	NNSDNAKIYINGKLESNIDIKDIGEVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTESQ	1068
Query: 243	SNIEERYKIQSSEYLKDFWGNPLMYNKEYMFNAGNKN SYIKLKKDSPGEILTRSKYN SNI+E YKIQSSEYLKDFWGNPLMYNKEYMFNAGNKN SYIKLKKD VGEILTRSKYN	302
Sbjct: 1069	SNIKEIYKIQSSEYLKDFWGNPLMYNKEYMFNAGNKN SYIKLKKDSSVGEILTRSKYN	1128
Query: 303	QNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYXXXXXX QMS XINYR+LYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFF N+EWNVX	362
Sbjct: 1129	QNSNYINYRNLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNSNREWRVYAYKDFKE	1188
Query: 363	XXXXXXXXAPISDSDEFYNTIQIKEYDEQPTYSQLLFKKDEESTDEIGLIGHRFYESGI A I DS+EFY TIQIKEYDEQPTYSQLLFKKDEESTDEIGLIGHRFYESGI	422
Sbjct: 1189	EEKKLFLANIYDSNEFYKTIQIKEYDEQPTYSQLLFKKDEESTDEIGLIGHRFYESGI	1248
Query: 423	VFEEYKDYFCISKWYLKEVKRKPYNLKGNCNWQFIPKDEGWTE V ++YK+YFCISKWYLKEVKRKPYNLKGNCNWQFIPKDEGW E	465
Sbjct: 1249	VLKDYKNYFCISKWYLKEVKRKPYNPNLGCNCNWQFIPKDEGWIE	1291

Score = 800 bits (2067), Expect = 0.0
Identities = 387/463 (83%), Positives = 416/463 (89%)

Query: 3	NKYLKTIMPFDLSIYTNDTILIEMFNKNYNEXXXXXXXXXRYKDNNLIDLSSGYGAKVEVY	62
	+KYLNKI+PFDSL Y+N ILI++FNKYNSE RY+DNNLIDLSSGYGAKVEVY	
Sbjct: 829	DKYLKTIIPFDLSTYSNIEILIKIFNKYNSEILNNIILNLRYRDNNLIDLSSGYGAKVEVY	888
Query: 63	DGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFDFSVSFWIRIPKYKNDGIQNYIHN	122
	DGV+LNDKNQFKLTSSA+SKIRVTQNQNIIFNS+FLDFSVSFWIRIPKY+ND IQNYIHN	
Sbjct: 889	DGVKLNDKNQFKLTSSADSKIRVTQNQNIIFNSMFLDFSVSFWIRIPKYRNDIQtyIHN	948
Query: 123	EYTIINCMKNNSGWKISIRGNRIWTLDINGKTKSVFFEYNIREDISEYINRWFFVTIT	182
	EYTIINCMKNNSGWKISIRGNRIWTLDINGKTKSVFFEYNIREDISEYINRWFFVTIT	
Sbjct: 949	EYTIINCMKNNSGWKISIRGNRIWTLDINGKTKSVFFEYNIREDISEYINRWFFVTIT	1008
Query: 183	NNLNNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQ	242
	NNL+NAKIYING LESN DIKDI EVI NGEI FKLDGD+DRTQFIWMKYFSIFNTELSQ	
Sbjct: 1009	NNLDNAKIYINGTLESNMDIKDIGEVIVNGEITFKLDGDVDRQFIWMKYFSIFNQLNQ	1068
Query: 243	SNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKN SYIKLKKDSPVGEILTRSKY	302
	SNI+E YKIGSYSEYLKDFWGNPLMYNKEYYMFNAGNKN SYIKL KDS VGETL PSKY	

+K+LKTII+PFDSL+S+YTN+TILIE+FNKYNSE RY+DNNILIDLSGYGA VEVY 888
Sbjct: 829 DKHLKTIIPFDLSMYTNNTILIEIFNKYNSEILNNIILNLRYRDNNLIDLSGYGANVEVY 888

DGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSWSFWIRIPKYKNDGIQNYIHN 122
Query: 63 DGVELNDKNQFKLTSS NS+IRVTQNQNIIFNS+FLDFSVSFWRIPKYKNDGIQNYIHN 122

DGVELNDKNQFKLTSSTNSEIRVTQNQNIIFNSMFLDFSVSFWRIPKYKNDGIQNYIHN 948
Sbjct: 889 DGVELNDKNQFKLTSSTNSEIRVTQNQNIIFNSMFLDFSVSFWRIPKYKNDGIQNYIHN 948

EYTIINC MKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTIT 182
Query: 123 EYTIINC+KNNSGWKISIRGNRIIWTL DINGKTKSVFFEY+TREDIS+YTNRWFFVTIT 182

EYTIINC KNNSGWKISIRGNRIIWTLTDINGKTKSVFFEYSIREDISDYINRWFFVTIT 1008
Sbjct: 949 EYTIINC KNNSGWKISIRGNRIIWTLTDINGKTKSVFFEYSIREDISDYINRWFFVTIT 1008

NNLNNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQ 242
Query: 183 NN +NAKIYINGKLESN DIKDI EVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQ 242

NNSDNAKIYINGKLESNIDIKDIGEVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQ 1068
Sbjct: 1009 NNSDNAKIYINGKLESNIDIKDIGEVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQ 1068

SNIERYKIQSSEYLKDFWGNPLMYNKEYMFNAGNKN SYIKLKKDSPGEILTRSKYN 302
Query: 243 SNI+E YKIQSSEYLKDFWGNPLMYNKEYMFNAGNKN SYIKLKKDSSVGEILTRSKYN 302

SNIKEIYKIQSSEYLKDFWGNPLMYNKEYMFNAGNKN SYIKLKKDSSVGEILTRSKYN 1128
Sbjct: 1069 SNIKEIYKIQSSEYLKDFWGNPLMYNKEYMFNAGNKN SYIKLKKDSSVGEILTRSKYN 1128

QNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYXXXXXX 362
Query: 303 QMS YINYR+LYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFN N+EWRVY 362

QNSNYINYRNLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNSNREWRYAYKDFKE 1188
Sbjct: 1129 QNSNYINYRNLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNSNREWRYAYKDFKE 1188

XXXXXXXXAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGHRFYESGI 422
Query: 363 A I DS+EFT TIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGHRFYESGI 422

EEKKLFLANIYDSNEFYKTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGHRFYESGI 1248
Sbjct: 1189 EEKKLFLANIYDSNEFYKTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGHRFYESGI 1248

VFEEYKDYFCISKWYLKEVKRKPYNLKGNCNWQFIPKDEGWTE 465
Query: 423 V ++YK+YFCISKWYLKEVKRKPYNLKGNCNWQFIPKDEGW E 465

VLKDYKNYFCISKWYLKEVKRKPYNPNLGCNWOFIPKDEGWIE 1291
Sbjct: 1249 VLKDYKNYFCISKWYLKEVKRKPYNPNLGCNWOFIPKDEGWIE 1291

Score = 800 bits (2067), Expect = 0.0
Identities = 387/463 (83%), Positives = 416/463 (89%)

Query: 3	NKYLKTIMPFDLSIYTNDTILIEMFNKNYNEXXXXXXXXXRYKDNNNLIDLSSGYGAKVEVY	62
	+KYLISTI+PFDLS Y+N ILI++FNKYNSE RY+DNNNLIDLSSGYGAKVEVY	
Sbjct: 829	DKYLKTIIPFDLSTYSNIEILIKIFNKYNSEILNNIILNLRYRDNNLIDLSSGYGAKVEVY	888
Query: 63	DGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLLDFSVSFWIRIPKYKNDGQNYIHN	122
	DGV+LNQFKLTSSA+SKIRVTQNQNIIFNS+FLDFSVSFWIRIPKY+ND IONYIHN	
Sbjct: 889	DGVKLNDKNQFKLTSSADSKIRVTQNQNIIFNSMFLDFSVSFWIRIPKYRNDDQNYIHN	948
Query: 123	EYTIINCMKNNSGWKISIRGNRIWTLDINGKTKSVFFEYNIREDISEYINRWFFVTIT	182
	EYTIINCMKNNSGWKISIRGNRIWTLDINGKTKSVFFEYNIREDISEYINRWFFVTIT	
Sbjct: 949	EYTIINCMKNNSGWKISIRGNRIWTLDINGKTKSVFFEYNIREDISEYINRWFFVTIT	1008
Query: 183	NNLNNNAKIYINGKLESNTDIKDIREVIANGEIIIFKLDGDIDRTQFIWMKYFSIFNTELSQ	242
	NNL+NAKIYING LESN DIKDI EVI NGEI FKLDGD+DRTQFIWMKYFSIFNTELSQ	
Sbjct: 1009	NNLDNAKIYINGTLESNMDIKDIGEVIVNGEITFKLDGDVDRQFIWMKYFSIFNTELSQ	1068
Query: 243	SNIEERYKIQSYSEYLKDFWGNPLMYNKEYMFNAGNKNSYIKLKKDSPVGEILTRSKYN	302
	SNI+E YKICGSYSEYLKDFWGNPLMYNKEYMFNAGNKNSYIKL KDS VGEIL PSKYN	

Sbjct: 1069 SNIKEIYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKN SYIKLVKDSSVGEILIRSKYN 1128

Query: 303 QNSKYINYRDLYIGEKFIIIRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRYXXXXXX 362
QNS YINYR+LYIGEKFIIIRR+SNSQSINDDIVRKEDYI+LD ++EWRVY

Sbjct: 1129 QNSNYINYRNLYIGEKFIIIRRESNSQSINDDIVRKEDYIHL DLLHHEWRVYAYKYFKE 1188

Query: 363 XXXXXXXXAPISDSDEFYNTIQIKEYDEQPTYS CQLL FKDEESTDEIGLIGIHRFYESGI 422
+ ISDS+EYF T I+IKEYDEQF+YS CQLL FKDEESTD+IGLIGIHRFYESG+

Sbjct: 1189 QEEKLFLSIIISDSNEFYKTIEIKEYDEQPSYSCQLL FKDEESTDDIGLIGIHRFYESGV 1248

Query: 423 VFEEYKDYFCISKWYLKEVKRKPYNLKG C N WQFIPKDEGWTE 465
+ ++YKDYFCISKWYLKEVKRKPY LG C N WQFIPKDEGWTE

Sbjct: 1249 LRKKYKDYFCISKWYLKEVKRKPYKSNLGC N WQFIPKDEGWTE 1291

tr Q9X708 Botulinum neurotoxin type B (Fragment) [boNT/B] 441
Q9X708_CLOBO [Clostridium
botulinum] AA
align

Score = 791 bits (2043), Expect = 0.0
Identities = 385/441 (87%), Positives = 402/441 (90%)

Query: 17 YTNDTILIEMFN KYNSEX XXXXXX RYKDNN LIDL SGYGA KVEVYDGVELNDKNQFKLT 76
YT N+TILIE+FN KYN S+ RY+DNN LIDL SGYGA VEVYDGVELNDKNQFKLT
Sbjct: 1 YTNN TILIE IFN KYN SKI LNN I LNL RYRDNN LIDL SGYGA NVEVYDGVELNDKNQFKLT 60

Query: 77 SSANSKIRVTQNQNIIFNSVFLDFSVSF WIRIPK YKNDG I QNYIHNEYTIINC MKN NSGW 136
SS NS+IRVTQNQNIIFNS+FLDFSVSF WIRIPK YKNDG I QNYIHNEYTIINC+KNNSGW
Sbjct: 61 SSTNSEIRVTQNQNIIFNSMFLDFSVSF WIRIPK YKNDG I QNYIHNEYTIINC IKN NSGW 120

Query: 137 KISIRGNRIIWTLIDINGKTKSVFF EYNIREDISEYI NRWF FVTITNNLNNAKIYINGKL 196
KISIRGNRIIWTL DINGKTKSVFF EY+TREDIS+YI NRWF FVTITNN +NAKIYINGKL
Sbjct: 121 KISIRGNRIIWTLTDINGKTKSVFF EY SIREDISDYI NRWF FVTITNNSDNAKIYINGKL 180

Query: 197 ESN TDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQS NIEERYKIQSYSE 256
ESN DIKDI EVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNT+E YKIQSYSE
Sbjct: 181 ESNIDIKD IGEVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIKEIYKIQSYSE 240

Query: 257 YLKDFWGNPLMYNKEYYMFNAGNKN SYIKL KK DS PVGEILTRSKY N QNSK YIN YRDLYIG 316
YLKDFWGNPLMYNKEYYMFNAGNKN SYIKL KK DS VGEILTRSKY N QNS YIN YR+LYIG
Sbjct: 241 YLKDFWGNPLMYNKEYYMFNAGNKN SYIKL KK DS VGEILTRSKY N QNSK YIN YRNLYIG 300

Query: 317 EKFIIRRK SNSQSINDDIVRKEDYIYLDFFNLNQEWRYXXXXXXXXXAPISDS 376
EKFIIRRK SNSQSINDDIVRKEDYIYLDFFN N+EWRVY A I DS+
Sbjct: 301 EKFIIRRK SNSQSINDDIVRKEDYIYLDFFNSNREWRVYAYKDFKEEEKLV LANIYDSN 360

Query: 377 EFYNTIQIKEYDEQPTYS CQLL FKDEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKW 436
EFY T I+IKEYDEQPTYS CQLL FKDEESTDEIGLIGIHRFYESGIV ++YK+YFCISKW
Sbjct: 361 EFYKTIQIKEYDEQPTYS CQLL FKDEESTDEIGLIGIHRFYESGIVLKD YKN YFCISKW 420

Query: 437 YLKEVKRKP YNLKG C N WQFI 457
YLKEVKRKP YN LG C N WQFT
Sbjct: 421 YLKEVKRKP YNP NLGC N WQFI 441

Sbjct: 1069 SNIKEIYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKN SYIKLVKDSSVGEILIRSKYN 1128

Query: 303 QNSKYINYRDLYIGEKFII RKSNSQSINDDIVRKEDYIYLDFFNLNQEWRYTXXXXXX 362
QNS YINYR+LYIGEKFII R+SNSQSINDDIVRKEDYI+LD ++EWK VY

Sbjct: 1129 QNSNYINYRNLYIGEKFII RRESNSQSINDDIVRKEDYIHL DLLVHHEEWRYAYKYFKE 1188

Query: 363 XXXXXXAPISDSDEFYNTIQIKEYDEQPTYS CQLL FK DEESTDEIGLIGIHRFYESGI 422
+ ISDS+EFY TI+IKEYDEQP+YS CQLL FK DEESTD+IGLIGIHRFYESG+

Sbjct: 1189 QEEKLFLSII SNEFYKTIEIKEYDEQPSYSCQLL FK DEESTDDIGLIGIHRFYESGV 1248

Query: 423 VFEEYKDYFCISKWLKEVKRKPYNLKG C NWQFIPKDEGWTE 465
+ ++YKDYFCISKWLKEVKRKPY LG C NWQFIPKDEGWTE

Sbjct: 1249 LRKKYKDYFCISKWLKEVKRKPYKSNLGC NWQFIPKDEGWTE 1291

tr Q9X708 Botulinum neurotoxin type B (Fragment) [boNT/B] 441
Q9X708_CLOBO [Clostridium AA
botulinum] align

Score = 791 bits (2043), Expect = 0.0
Identities = 385/441 (87%), Positives = 402/441 (90%)

Query: 17 YTNDTILIE MFN KYN SE XXXXXX RY KDN NL ID LSGY GAK VEV YDG VEL ND KNQ FK LT 76
YT N+T I LIE+ F N K Y N S+ RY+D N N L I D L S G Y G A V E V Y D G V E L N D K N Q F K L T
Sbjct: 1 YTN NT I LIE I F N K Y N S K I L N N I I L N L R Y R D N N L I D L S G Y G A N V E V Y D G V E L N D K N Q F K L T 60

Query: 77 SSANSKIRVTQNQNIIFNSVF LDFS VFWIRIPKYKNDG I QNYIHNEYTIINC MKNN SGW 136
SS NS+I R VT QN QN I IF NS+FL D F SV F W I R I P K Y K N D G I Q N Y I H N E Y T I I N C +K N N S G W
Sbjct: 61 SSTNSEIRVTQNQNIIFNSMFLDFSVF WIRIPKYKNDG I QNYIHNEYTIINC I K N N SGW 120

Query: 137 KISIRGNRIIWTLIDINGKTKSVFF EYNIREDISEYINRWFFVTITNNLNNAKIYINGKL 196
KISIRGNRIIWTL DINGKTKSVFF EY+TREDIS+YINRWFFVTITNN +NAKIYINGKL
Sbjct: 121 KISIRGNRIIWTLTDINGKTKSVFF EYSIREDISDYINRWFFVTITNNSDNAKIYINGKL 180

Query: 197 ESNTDIK DIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNT ELSQS NIEERYKIQSYSE 256
ESN DIK DIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNT ELSQS NIEERYKIQSYSE
Sbjct: 181 ESNIDIK D IGEVIANGEIIFKLDGDIDRTQFIWMKYFSIFNT ELSQS NIKEIYKIQSYSE 240

Query: 257 YLKDFWGNPLMYNKEYYMFNAGNKN SYIKL KK DS PV GEILTRSKY N QNSK YIN Y RDLYIG 316
YLKDFWGNPLMYNKEYYMFNAGNKN SYIKL KK DS VGEILTRSKY N QNS YIN YR+LYIG
Sbjct: 241 YLKDFWGNPLMYNKEYYMFNAGNKN SYIKL KK DS PV GEILTRSKY N QNSK YIN YR NLYIG 300

Query: 317 EKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRYTXXXXXXXXXAPISDSD 376
EKFIIRRKSNSQSINDDIVRKEDYIYLDFFN N+EWRY A I DS+
Sbjct: 301 EKFIIRRKSNSQSINDDIVRKEDYIYLDFFNSNREWRVYAYKDFKEEEKLV LANIYDSN 360

Query: 377 EFYNTIQIKEYDEQPTYS CQLL FK DEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKW 436
EFY TI+IKEYDEQPTYS CQLL FK DEESTDEIGLIGIHRFYESGIV ++YK+YFCISKW
Sbjct: 361 EFYKTIQIKEYDEQPTYS CQLL FK DEESTDEIGLIGIHRFYESGIVLKD YKNYFCISKW 420

Query: 437 YLKEVKRKP YNLKG C NWQFI 457
YLKEVKRKP YNLKG C NWQFI
Sbjct: 421 YLKEVKRKP YNP NLGC NWQFI 441

sp Q60393 Botulinum neurotoxin type G precursor (EC 3.4.24.69) 1296
 BXG_CLOBO (BoNT/G) (Bontoxilysin G) [botG] [Clostridium botulinum] AA align

Score = 468 bits (1203), Expect = e-130
 Identities = 230/469 (49%), Positives = 324/469 (69%), Gaps = 11/469 (2%)

Query: 3 NKYLKTIMPFDSLITYTNDTILIEFMNKYNSEXXXXXXXXRYKDNNNLIDLSGYGAKVEVY 62
 N++LK +PFDSL+YT DTTLI++FN Y S Y+ LWD SGYGA + V
 Sbjct: 833 NRHLKDSIPFDLSLYTAKDTILQVFNNYISNISSNAILSLSYRGGRLLIDSSGYGATMNVG 892

Query: 63 DGVELND--KNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYI 120
 V NC QFKL +S NS I Q++ +++++S+F +FS++FW+R PKY N+ EQ Y+
 Sbjct: 893 SDVIFNDIGNGQFKLNNSENSNITAHQSKFVVYDSMFDNFSINFWRTPKYNNDIQTYL 952

Query: 121 HNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVT 180
 NEYTI+C+KN+SGWK+ST+GNRIIWTFLID+N K+KS+FFEY+I+I+IS+YIN+WF +T
 Sbjct: 953 QNEYTIISCIKNDSGWKVSIKGRIIWTLIDVNAKSksIFFEYSIKDNISDYINKWFSIT 1012

Query: 181 ITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIIFKLDGDIDRTQFIWMKYFSIFNTE 239
 ITN+ I MA IYING L+ + I ++ + * + I FKL D T+F+W+K F+IF E
 Sbjct: 1013 ITNDRLGNANIYINGSLKKSEKILNLDRINSSNDIFKLINCTDTKFVWIKDFNIFGRE 1072

Query: 240 LSQSNEERYKIQSYSSEYLKDFWGPNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGELTRS 299
 L+ + + Y IGS + LKDFWGPNPL Y+ +YY+FN G +N YIN + +GE R+
 Sbjct: 1073 LNATEVSSLWIQSSTNTLKDFWGPNPLRYDTQYYLFNQGMQNIYIKYFSKASMGETAPRT 1132

Query: 300 KYNQNSKYINYRDLYIGEKFIIRRKSNSQSI-NDDIVRKEDYIYLDFFNLNQE-WRVYTX 357
 +N + INY++LY+G +TII++ SNS++I ND+IVR+ DTYL+ N++ E +RVY
 Sbjct: 1133 NFNNAA--INYQONLYGLRFIIKKASNSRNINNDNIVREGDYIYLNIDNISDESYRVYVL 1190

Query: 358 XXXXXXXXXXXXAPISDSDEFYNTIQIKEYDEQPTYSQQLFKKDEESTDEIGLIGIHRF 417
 API+D FY+ +QIK+Y E+ TY+CQ+L +KD T GL GT +F
 Sbjct: 1191 VNSKEIQTQLFLAPINDDPTFYDVLQIKKYYEKTTYNCQILCEKD---TKTFGLFGIGKF 1247

Query: 418 YES-GIVFEEYKDYFCISWKYLKEVKRKPYNLKGNCNWQFIPKDEGWTE 465
 + G V++ Y +YFCIS+WYL+ + D+LGNCNWQFIP DEGWTE
 Sbjct: 1248 VKDYGYVWDTYDNYFCISQWYLRRISENINKLRLGCNCNWQFIPVDEGWTE 1296

sp P10845 Botulinum neurotoxin type A precursor (EC 3.4.24.69) 1295
 BXA1_CLOBO (BoNT/A) (Botox) [Contains: Botulinum neurotoxin AA align
 A light-chain; Botulinum neurotoxin A heavy-chain] [botA]
 [Clostridium botulinum]

Score = 316 bits (810), Expect = 6e-85
 Identities = 182/476 (38%), Positives = 265/476 (55%), Gaps = 37/476 (7%)

Query: 3 NKYLKTIMPFDSLITYTNDTILIEFMNKYNSEXXXXXXXXRYKDNNNLIDLSGYGAKVEVY 62
 N L T +PF LS Y ++ L+ F +Y RY+ N+LIDLS Y +K+ +
 Sbjct: 841 NNTLSTDIPFQLSKYVDNQRLSTFTEYIKNIINTSILNRLYESNHLIDLSRYASKINIG 900

Query: 63 DGVELN--DKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYI 120
 V + DKNQ +I + +SKI V I++NS++ +FS SFWIRIPKY N N
 Sbjct: 901 SKVNFDPIDKNQIQLFNLESSKIEVILKNAIVYNSMYENFSTSFWIRIPKYFNSISLN-- 958

sp Q60393 Botulinum neurotoxin type G precursor (EC 3.4.24.69) 1296
 BXG_CLOBO (BoNT/G) (Bontoxilysin G) [botG] [Clostridium botulinum] AA align

Score = 468 bits (1203), Expect = e-130
 Identities = 230/469 (49%), Positives = 324/469 (69%), Gaps = 11/469 (2%)

Query: 3 NKYLKTIMPFDLSIYTNDTILIEFMNKYNSEXXXXXXXXXRYKDNNLIDLSGYAKVEVY 62
 N++LK +PFDSL+YT DTIELI++FN Y S Y+ N+LID SGYGA + V
 Sbjct: 833 NRHLKDSIPFDLSLYTKDTILIQVFNNYISNISSNAILSLSYRGGRIDLSSGYGATMNVG 892

Query: 63 DGVELND--KNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYI 120
 V ND QFKL +S NS I Q++ +++++F +FS++FW+F PKY N+ TQ Y+
 Sbjct: 893 SDVIFNDIGNQFKLNNSENSNITAHQSKFVYDSMFDNFSINFWVTPKYNNDIQTYL 952

Query: 121 HNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVT 180
 NEYTI+I+C+KN+SGWK+SI+GNRIIWTLID+N K+KS+FFEY+I++FIS+YIN+WF +T
 Sbjct: 953 QNEYTIISCIKNDSGWKVSIKGRIIWTLIDVNAKSksIFFEYSIKDNISDYINKWFSIT 1012

Query: 181 ITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIIFKLDGDIDRTQFIWMKYFSIFNTE 239
 ITN+ I NA IYING L+ + I ++ + ++ +I EKI D T+F+WF E+IF E
 Sbjct: 1013 ITNDRLLGNANIYINGSLLKSEKILNLDRINSSNDIFKLINCTDTKFVWIKFNFNIFGRE 1072

Query: 240 LSQSNIIEERYKIQSYSEYLKDFWGPNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRS 299
 I+ + + Y IQS + LKDFWGPNPL Y+ +YY+FN G +N YIK + +GE R+
 Sbjct: 1073 LNATEVSSLYWIQSSTNTLKDFWGPNPLRYDTQYYLFNQGMQNIYIKYFSKASMGETAPRT 1132

Query: 300 KYNQNSKYINYRDLYIGEKFIIRRKSNSQSI-NDDIVRKEDYIYLDFFNLNQE-WRVYTX 357
 +N + INY++LY+G +WII++ SNS++I ND+IVK+ DYIYL+ N++ E +RVY
 Sbjct: 1133 FNFNAA--INYQONLYLGLRFIIKKASNSRNINNDNIVREGDYIYLNIDNISDESYRVYVL 1190

Query: 358 XXXXXXXXXXXXAPISDSDEFYNTIQIKEYDEQPTYSCQLLFFKKDEESTDEIGLIGHRF 417
 API+D FY+ +QK+Y E+ TY+CQ+L +KD P GL GT +F
 Sbjct: 1191 VNSKEIQTQLFLAPINDDPTFYDVLQIKKYYEKTTCNCQILCEKD---TKTFGLFGIGKF 1247

Query: 418 YES-GIVFEEYKDYFCISKWYLKEVKRKPYNLKLCNWQFIPKDEGWTE 465
 + G V++ Y +YFCIS+WYL+ + L+LGCNWQFIP DEGWTE
 Sbjct: 1248 VKDYGYVWDTYDNYFCISQWYLRRISENINKRLGCNWQFIPVDEGWTE 1296

sp P10845 Botulinum neurotoxin type A precursor (EC 3.4.24.69) 1295
 BXA1_CLOBO (BoNT/A) (BOTOX) [Contains: Botulinum neurotoxin A light-chain; Botulinum neurotoxin A heavy-chain] [botA] [Clostridium botulinum] AA align

Score = 316 bits (810), Expect = 6e-85
 Identities = 182/476 (38%), Positives = 265/476 (55%), Gaps = 37/476 (7%)

Query: 3 NKYLKTIMPFDLSIYTNDTILIEFMNKYNSEXXXXXXXXXRYKDNNLIDLSGYAKVEVY 62
 N L T +PF LS Y ++ L+ F *Y RY+ N+LIDLS Y +K+ *
 Sbjct: 841 NNTLSTDIPFQLSKYVDNQRLLSTFTEYIKNIINTSILNRLYESNHLIDLSRYASKINIG 900

Query: 63 DGVELN--DKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYI 120
 V + DKNQ +L + +SKI V I++N3++ +FS SFWIRIPKY N N
 Sbjct: 901 SKVNFDPIDKNQIQLFNLESSKIEVILKNAIVYNSMYENFSTSFWIRIPKYFNSISLN-- 958

Query: 121 HNEYTIINCMKNNSGWKISIRGNRIIWTLLIDINGKTKSVFFEYNIREDISEYINRWFFVT 180
NEYTIINCM+NNSGWK+S+ IIWTL D + V F+Y+ +IS+YTNRW FVT
Sbjct: 959 -NEYTIINCMENNSGWVSLNYGEIIWTLQDTQEIKQRVVFKYSQMINISDYINRWIFVT 1017

Query: 181 ITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTE 239
ITNN LNN+KIYING+L T ++ + A+ I+FKLDG D ++IW+KVYF++E+ E
Sbjct: 1018 ITNNRLLNNSKIYINGRLIDQKPISNLGNIHASNINMFKLDGCRDTHRYIWIKYFNLFDE 1077

Query: 240 LSQSNIIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKK-----DS 290
L++ I++ Y QS S LKDFWG+ L Y+K YYM N + N Y+ +
Sbjct: 1078 LNEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKYVDVNVGIRGYMLKG 1137

Query: 291 PVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQ 350
P G ++T + Y +S LY G KFII++ ++ D+IVR D +Y++ N+
Sbjct: 1138 PRGSVMTTNIYLNSS-----LYRGTKFIKKYASGN--KDNIVRNNDRVYINVVKNK 1188

Query: 351 EWRYVXXXXXXXXXXXXXAPISDSDEFYNTIQIKEYDEQP-TYSCQLLFKKDEESTDEI 409
E+R+ T I D + +K +++Q T C++ + + ++I
Sbjct: 1189 EYRLATNASQAGVEKILSALEIPDVGNLSQVVMKSKNDQGITNKCKM--NLQDNNGNDI 1246

Query: 410 GLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKGNCNWQFIPKDEGWTE 465
G IG H+F S WY +++R + LGC+W+P+P D+GW E
Sbjct: 1247 GFIGFHQFNNIA-----KLVASNWYNRQIERS--SRTLGCSEWEFIPVDDGWGE 1292

tr Q7B8V4 BoNT/A [bont/a] [Clostridium botulinum] 1296 AA
Q7B8V4 CLOBO align

Score = 316 bits (810), Expect = 6e-85
Identities = 182/476 (38%), Positives = 265/476 (55%), Gaps = 37/476 (7%)

Query: 3 NKYLKТИMPFDLSIYTNDTILIEMFNКYNSEXXXXXXRYKDNNLIDLSGYGAKVEVY 62
N L T +PF LS Y ++ L+ F +Y RY+ N+LIDLX X +R+ +
Sbjct: 842 NNTLSTDIPFQLSKYVDNQRLLSTFTEYIKNIINTSILNLRYESNHLIDLSRYASKINIG 901

Query: 63 DGVELN--DKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYI 120
V + DKNQ +L + +SKT V I++NS++ +FS SFWIRIPKY N N
Sbjct: 902 SKVNFDPIDKNOIQLEFNLESSKIEVILKNAIVYNSMYENFSTSFWIRIPKYFNSISLN-- 959

Query: 121 HNEYTIINC MKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVT 180
NEYTIINC M+NNSGWK+S+ IIWTL D + V F+Y+ +IS+YINKW FVT
Sbjct: 960 -NEYTIINC MENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYSQMINISDYINRWIFVT 1018

Query: 181 ITNN-LNNAKIYIYNGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTE 239
ITNN LNN+KIIYING+L I ++ + A+ I+FKLDG D +IW+KYF+ +F+ E
Sbjct: 1019 ITNNRLNNSKIYIYNGRLIDQKPISNLGNIASNNIMFKLDGCRDTHRYIWIKYFNLFDKE 1078

Query: 240 LSQSNIERYKIQSSEYLKDFWGNPLMYNKEYMFNAGNKN SYIKLKK-----DS 290
L++ I++ Y QS S LKDFWG+ I Y+K YYM N + N Y+ +
Sbjct: 1079 LNEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKYVDNNVGIRGYMYLK 1138

Query: 291 PVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLQ 350
P G ++T + Y +S LY G KFII++ ++ D+TVR D +Y++ N+
Sbjct: 1139 PRGSVMTTNIYLNSS-----LYRGTKFIKKYASGN--KDNIVRNNDRVYINVVKNK 1189

Query: 351 EWRYVYXXXXXXXXXXXXXAPISDSDEFYNTIQIKEYDEQP-TYSCQLLFKKDEESTDEI 409

Query: 121 HNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFV 180
NEYTIINCM+NNSGWK+S+ IIWTL D + V F+Y+ +IS+YTNRW FVT
Sbjct: 959 -NEYTIINCMENNSGWKVSLSNYGEIIWTLQDTQEIKQRVVFKYSQMINISDYINRWIFVT 1017

Query: 181 ITNN-LNAKIYINGKLESNTDIKDIREVIANGEIIFKLDG DIDRTQFIWMKYFSIFNTE 239
ITNN LNN+KIYING+L I ++ + A+ I+FKLDG D ++TW+KTF++F+ E
Sbjct: 1018 ITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDE 1077

Query: 240 LSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYMFNAGNKNSYIKLKK-----DS 290
L++ I++ Y QS S LKDFWG+ L Y+K YYM N + N Y+ +
Sbjct: 1078 LNEKEIKDLYDNQSNSGILKDFWDYLOYDKPYYMLNLYDPNKYVDVNNVGIRGYMLKG 1137

Query: 291 PVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQ 350
P G ++T + Y +S LY G KFI++ ++ D+IVR D +Y++ N+
Sbjct: 1138 PRGSVMTTNIYLNSS-----LYRGTKFIKKYASGN--KDNIVRNNDRVYINVVKNK 1188

Query: 351 EWRVYXXXXXXXXXXXXXAPISDSDEFYNTIQIKEYDEQP-TYSCQLLFKKDEESTDEI 409
E+R+ T I D + +K ++Q T C++ + + +E
Sbjct: 1189 EYRLATNASQAGVEKILSALEIPDVGNLSQVVVMKSNDQGITNKCKM--NLQDNNNGNDI 1246

Query: 410 GLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKGNCNWQFIPKDEGWTE 465
G IG H+F S WY ++++++R + LGC+W+FP D+GW E
Sbjct: 1247 GFIGFHQFNNIA-----KLVASNWYNQIERS--SRTLGCSWEFIPVDDGWGE 1292

tr Q7B8V4 BoNT/A [bont/a] [Clostridium botulinum] 1296 AA
Q7B8V4_CLOBO align

Score = 316 bits (810), Expect = 6e-85
Identities = 182/476 (38%), Positives = 265/476 (55%), Gaps = 37/476 (7%)

Query: 3 NKYLKTIMPFDSLISYTNDTILIEMFNKNSEXXXXXXXXXRYKDNNNLIDLSGYGAKVEVY 62
Sbjct: 842 NNTLSTDIPFQLSKYVDNQRLSTFTEYIKNIINTSILNRLYESNHLIDLSRYASKINIG 901

Query: 63 DGVELN--DKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVFWIRIPKYKNDGIQNYI 120
Sbjct: 902 V + DKNQ +L + +SKT V I++NS++ +FS SFWIRIPKY N N SKVNFDPIDKRNQIQLFNLESSKIEVILKNAIVYNSMYENFSTSFWIRIPKYFNSISLN-- 959

Query: 121 HNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTGSVFFEYNIREDISEYINRWFV 180
Sbjct: 960 NEYTIINCM+NNSGWK+S+ IIWTL D + V F+Y+ +IS+YINRW FVT -NEYTIINCMENNNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYSQMINISDYINRWFV 1018

Query: 181 ITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIIFKLDGDIDRTQFIWMKYFSIFNTE 239
Sbjct: 1019 ITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDKE 1078

Query: 240 LSQSNIEERYKIQSYSEYLKDFWGPNPLMYNKEYYMFNAGNKNNSYIKLKK-----DS 290
Sbjct: 1079 L++ I++ Y QS S LKDFWG+ L Y+K XYM N + N Y+ + LNEKEIKDLYDNQSNSGILKDFWGDLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKG 1138

Query: 291 PVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQ 350
Sbjct: 1139 P G ++T + Y +S LY G KFII++ ++ D+IVR D +Y++ N+ PRGSVMTTNIYLNSS-----LYRGTKFIKKYASGN--KDNIVRNNDRVYINVVVKNK 1189

Query: 351 EWRVYXXXXXXXXXXXXXAPISDSDEFYNTIQIKEYDEQP-TYSCQLLFKKDEESTDEI 409

E+R+ T I D + +K ++Q T C++ + + ++T
 Sbjct: 1190 EYRLATNASQAGVEKILSALEIPDVGNLSQLVVVMKSNDQGITNKCKM--NLQDNNGNDI 1247

Query: 410 GLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKGNCNWQFIPKDEGWTE 465
 G IG H+F S WY ++++R + LGC+W+FTP D+GW E
 Sbjct: 1248 GFIGFHQFNNIA-----KLVASNWYNRQIERS--SRTLGCSWEFIPVDDGWGE 1293

tr Q45851 Neurotoxin type F [bont /f] [Clostridium baratii] 1268 AA
Q45851_9CLOT align

Score = 301 bits (771), Expect = 2e-80
 Identities = 179/471 (38%), Positives = 270/471 (57%), Gaps = 32/471 (6%)

Query: 1 MANKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXRYKDNNLIDLGYGAKVE 60
 + + L +PF+LS YTND ILE + ++ +Y+NM ID SGYG+ +
 Sbjct: 824 LVSNTLNNSIPFELSEYTNDKILIHILIRFYKRIIDSSILNMKYENNRFIDSSGYGSNIS 883

Query: 61 VYDGVEL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWRIPKYKNDGIQN 118
 + + + ++NQF + SS S++ +TQN LI+NS + +FSVSEFW+RIPKY N ++N
 Sbjct: 884 INGDIYIYSTNRNQFGIYSSRLSEVNITQNNIIYNSRYQNFVSEFWVRIPKYNN--LKN 941

Query: 119 YIHNEYTIINCMKNN-SGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWF 177
 ++NEYTTINCM+NN SGWKIS+ N IIWTL D G + + F Y DIS+YTN+W
 Sbjct: 942 -LNNEYTIINCMRNNNSGWKISLNYYNNIWTLQDTTGNNQKLVFNYTQMDISDYINKWT 1000

Query: 178 FVTITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIF 236
 FVTITNN L ++K+YING L I ++ + * I+FK+ G D T+++ ++YF IF
 Sbjct: 1001 FVTITNNRLGHSKLYINGNLTQDKSILNLGNIHVDNNILFKIVGCND-TRYVGIRYFKIF 1059

Query: 237 NTELSQSNEERYKIQSSEYLKDWFGNPLMYNKEYMFNAGNKNYSIKLKKDSPVGEI- 295
 N EL ++ IE Y + S LKDFWGN L+YNN+XY+ N N + + K+S + I
 Sbjct: 1060 NMELDKTEIETLYHSEPDSTILKDFWGNYLLYNKYYLLNLLKPN--MSVTKNSDILNIN 1117

Query: 296 LTRSKYQNSKYINYRDLYIGEKFIIIRKSNSQSIN-DDIVRKEDYIYLDFFNLNQEWRV 354
 R Y++ + + N R LY G + IIR+ ++ + N D+ VRK D +Y++ + N E++
 Sbjct: 1118 RQRGIYSKTNIFSNAR-LYTGVIEVIIRKVGSTDTSNTDNFVRKNDTVYINVVDGNSEYQL 1176

Query: 355 YTXXXXXXXXXXXAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGI 414
 Y IS+S+ YN+ Q+ D +C + SK + + ++IGL+G
 Sbjct: 1177 YADVSTSAVEKTIKLRRISNSN--YNSNQMIIMDSIGD-NCTMFKTN--NGNDIGLLGF 1231

Query: 415 HRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKGNCNWQFIPKDEGWTE 465
 H + S WY K ++ N GC W FI K+ GW E
 Sbjct: 1232 H-----LNNLVASSWYYKNIRRNTRN--NGCFWSFISKEHWQE 1268

tr Q45846 Botulinum neurotoxin type B (Fragment) [BoNT/B] 361
Q45846_CLOBO [Clostridium botulinum] AA align

Score = 299 bits (765), Expect = 1e-79
 Identities = 144/166 (86%), Positives = 155/166 (92%)

Query: 3 NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXRYKDNNLIDLGYGAKVEVY 62

E+R+ T I D + +K ++Q T C++ + + + +T
 Sbjct: 1190 EYRLATNASQAGVEKILSALEIPDVGNLSQLVVVMKSNDQGITNKCKM--NLQDNNGNDI 1247

Query: 410 GLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKGNCNWQFIPKDEGWTE 465
 G IG H+F S W Y + + + +K + L G C + W + F T P D + G W E
 Sbjct: 1248 GFIGFHQFNNIA-----KLVASNWYNRQIERS--SRTLGCSWEFIPVDDGWGE 1293

tr Q45851 Neurotoxin type F [bont /f] [Clostridium baratii] 1268 AA
Q45851_9CLOT align

Score = 301 bits (771), Expect = 2e-80
 Identities = 179/471 (38%), Positives = 270/471 (57%), Gaps = 32/471 (6%)

Query: 1 MANKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXRYKDNNLIDLSGYGAKVE 60
 + + L +PF+LS YTND ILI + ++ +Y+NM ID SGYGF +
 Sbjct: 824 LVSNTLNNSIPFELSEYTNDKILIHILIRFYKRIIDSSILNMKYENNRFIDSSGYGSNIS 883

Query: 61 VYDGVEL--NDKNOFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWRIPKYKNDGIQN 118
 + + + + +NQF + SS S++ +TQN II+NS + +FSVCFW+RIPKY N + +N
 Sbjct: 884 INGDIYIYSTNRNQFGIYSSRLSEVNITQNNIIYNSRYQNFSVFWVRIPKYNN--LKN 941

Query: 119 YIHNEYTIINCMKNN-SGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWF 177
 + +NEYTTIINCM+NN SGWKIS+ N IIWTL D G + + F Y DIS+YEN+W
 Sbjct: 942 -LNNEYTIINCMRNNNSGWKISLNYYNNIIWTLQDTTGNNQKLVFNYTQMDISDYINKWT 1000

Query: 178 FVTITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIF 236
 FVTITNN L + +K+YING L I + + + + I+FK+ G D T++ + +YF IF
 Sbjct: 1001 FVTITNNRLGHSKLYINGNLTQDKSILNLGNIHVDNNILFKIVGCND-TRYVGIRYFKIF 1059

Query: 237 NTELSSQSNIEERYKIQSSEYLKDWFGNPLMYNKEYMFNAGNKNYSIKLKKDSPVGEI- 295
 N EL + + IE Y + S LKDFWGN L+YNN+YY+ N N + + K+S + I
 Sbjct: 1060 NMELDKTEIETLYHSEPDSTILKDFWGNYLLYNKKYLLNLLKPN--MSVTKNSDILNIN 1117

Query: 296 LTRSKYQNQSKYINYRDLYIGEKFIIIRKSNSQ SIN-DDIVRKEDYIYLDFFNLNQEWRV 354
 R Y++ + + N R LY G + IIR+ + + + N D+ VRK D +Y++ + N E+++
 Sbjct: 1118 RQRGIYSKTNIFSNAR-LYTGVIEVIRKVGSTDTSNTDNFVRKNDTVYINVVDGNSEYQL 1176

Query: 355 YTXXXXXXXXXXAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGI 414
 Y IS+S+ YN+ Q+ D +C + FK + + +IGL+G
 Sbjct: 1177 YADVSTSAVEKTIKLRRISNSN--YNSNQMIIMDSIGD-NCTMNFKTN--NGNDIGLLGF 1231

Query: 415 HRFYYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKGNCNWQFIPKDEGWTE 465
 H + S W Y K ++ N G C W F I K+ G W E
 Sbjct: 1232 H-----LNNLVASSWYYKNIRNNTRN--NGCFWSFISKEHWGE 1268

tr Q45846 Botulinum neurotoxin type B (Fragment) [BoNT/B] 361
Q45846_CLOBO [Clostridium botulinum] AA align

Score = 299 bits (765), Expect = 1e-79
 Identities = 144/166 (86%), Positives = 155/166 (92%)

Query: 3 NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXRYKDNNLIDLSGYGAKVEVY 62

+KYLKPI+PFDSL+YTN+ TLI++FNKYNS E RY+DNNLIDLSGYGAKVEVY
 Sbjct: 196 DKYLKTIIPFDLSMYTNNEILIKIFNKYNSEILNNIILNLRYRDNNLIDLSGYGAKVEVY 255

Query: 63 DGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHN 122
 UGV+LNQFKLTSSA+SKIRVTQNQNIIFNS+FLDFSVSFWIRIPKY+ND IQNYIHN

Sbjct: 256 DGVKLNDKNQFKLTSSADSKIRVTQNQNIIFNSMFLDFSVSFWIRIPKYRNDDIQNYIHN 315

Query: 123 EYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTCSVFFEYNIRED 168
 EYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTCSVFFEYNIRED

Sbjct: 316 EYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTCSVFFEYNIRED 361

tr Q45848 Botulinum neurotoxin type B (Fragment) [BoNT/B] 361
Q45848_CLOBO [Clostridium AA
 botulinum] align

Score = 298 bits (763), Expect = 2e-79
 Identities = 144/166 (86%), Positives = 154/166 (92%)

Query: 3 NKYLKTIIMPFDLSIYTNDTILIEFMNKYNSEXXXXXXXXRYKDNNLIDLSGYGAKVEVY 62
 +KYLKPI+PFDSL YTN+ TLI++FNKYNS E RY+DNNLIDLSGYGAKVEVY
 Sbjct: 196 DKYLKTIIPFDLSTYTNNNEILIKIFNKYNSEILNNIILNLRYRDNNLIDLSGYGAKVEVY 255

Query: 63 DGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHN 122
 UGV+LNQFKLTSSA+SKIRVTQNQNIIFNS+FLDFSVSFWIRIPKY+ND IQNYIHN

Sbjct: 256 DGVKLNDKNQFKLTSSADSKIRVTQNQNIIFNSMFLDFSVSFWIRIPKYRNDDIQNYIHN 315

Query: 123 EYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTCSVFFEYNIRED 168
 EYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTCSVFFEYNIRED

Sbjct: 316 EYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTCSVFFEYNIRED 361

sp Q45894 Botulinum neurotoxin type A precursor (EC 3.4.24.69) 1295
BXA2_CLOBO (BoNT/A) AA
 (Bontoxilysin A) (BOTOX) [Contains: Botulinum neurotoxin align
 A light-chain; Botulinum neurotoxin A heavy-chain] [botA]
 [Clostridium botulinum]

Score = 297 bits (761), Expect = 3e-79
 Identities = 175/475 (36%), Positives = 259/475 (53%), Gaps = 35/475 (7%)

Query: 3 NKYLKTIIMPFDLSIYTNDTILIEFMNKYNSEXXXXXXXXRYKDNNLIDLSGYGAKVEVY 62
 N L +PF LS Y ++ L+ F +Y YK ++LIDLS YGAK+ +
 Sbjct: 841 NNTLSADIPFQLSKYVDNKKLLSTFTEYIKNIVNTSILSIVYKKDDLIDLSRYGAKINIG 900

Query: 63 DGVELN--DKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYI 120
 D V + DKNQ K + +S I V T++NS++ +FG SFWI+IPKY + + +
 Sbjct: 901 DRVYYDSIDKNQIKLINLESSTIEVILKNAIVYNSMYENFSTSFWIKIPKYFS---KINL 957

Query: 121 HNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTCSVFFEYNIREDISEYINRWFV 180
 +NEYTIINC++NNSGWK+S+ IIWTL D + V F+Y+ +IS+YINRW FV
 Sbjct: 958 NNEYTIINCIENNNSGWKVSLNYGEIIWTLQDNKQNIQRVVFKYSQMVNISDYINRWFV 1017

Query: 181 ITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTE 239
 ITNN L +KIXING+L I ++ + A+ +T+EKLDG D + +I +KYF+ +F+ E

+KYLKTI+PFDSL+YTN+ TLT++FNKYNSE RY+DNMLIDLSGYGAKVEVY
 Sbjct: 196 DKYLKTIIPFDLMSYTNNELIKIFNKYNSEILNNIILNLRYRDNNLIDLSGYGAKVEVY 255

Query: 63 DGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVFWIRIPKYKNDGIQNYIHN 122
 DGV+LNDKNQFKLTSSA+SKIRVTQNQNIIFNS+FLDFSVFWIRIPKY+ND IQNYIHN
 Sbjct: 256 DGVKLNDKNQFKLTSSADSKIRVTQNQNIIFNSMFLDFSVFWIRIPKYRNDDIQNYIHN 315

Query: 123 EYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTGSVFFEYNIRED 168
 EYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTGSVFFEYNIRED
 Sbjct: 316 EYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTGSVFFEYNIRED 361

tr Q45848 Botulinum neurotoxin type B (Fragment) [BoNT/B] 361
Q45848_CLOBO [Clostridium AA
 botulinum] align

Score = 298 bits (763), Expect = 2e-79
 Identities = 144/166 (86%), Positives = 154/166 (92%)

Query: 3 NKYLKTIIMPFDLSIYTNDTILIEFMNKYNSEX XXXXXXXXRYKDNNLIDLSGYGAKVEVY 62
 +KYLKTI+PFDSL YTN+ TLT++FNKYNSE RY+DNMLIDLSGYGAKVEVY
 Sbjct: 196 DKYLKTIIPFDLSTYTNNELIKIFNKYNSEILNNIILNLRYRDNNLIDLSGYGAKVEVY 255

Query: 63 DGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVFWIRIPKYKNDGIQNYIHN 122
 DGV+LNDKNQFKLTSSA+SKIRVTQNQNIIFNS+FLDFSVFWIRIPKY+ND IQNYIHN
 Sbjct: 256 DGVKLNDKNQFKLTSSADSKIRVTQNQNIIFNSMFLDFSVFWIRIPKYRNDDIQNYIHN 315

Query: 123 EYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTGSVFFEYNIRED 168
 EYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTGSVFFEYNIRED
 Sbjct: 316 EYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTGSVFFEYNIRED 361

sp Q45894 Botulinum neurotoxin type A precursor (EC 3.4.24.69) 1295
BXA2_CLOBO (BoNT/A) AA
 (Bontoxilysin A) (BOTOX) [Contains: Botulinum neurotoxin align
 A light-chain; Botulinum neurotoxin A heavy-chain] [botA]
 [Clostridium botulinum]

Score = 297 bits (761), Expect = 3e-79
 Identities = 175/475 (36%), Positives = 259/475 (53%), Gaps = 35/475 (7%)

Query: 3 NKYLKTIIMPFDLSIYTNDTILIEFMNKYNSEX XXXXXXXXRYKDNNLIDLSGYGAKVEVY 62
 N L +PF LS Y ++ L+ F +Y YK ++LIDLS YGAK+ +
 Sbjct: 841 NNTLSADIPFQLSKYVDNKKLLSTFTEYIKNIVNTSILSIVYKKDDLIDLSRYGAKINIG 900

Query: 63 DGVELN--DKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVFWIRIPKYKNDGIQNYI 120
 D V + DKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVFWIRIPKYKNDGIQNYI
 Sbjct: 901 DRVYYDSIDKNQIKLINLESSTIEVILKNAIVYNSMYENFSTSFWIKIPKYFS---KINL 957

Query: 121 HNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTGSVFFEYNIREDISEYINRWFV 180
 +NEYTIINC++NNSGWK+S+ IIWTL D + V F+Y+ +IS+YINRW FV
 Sbjct: 958 NNEYTIINCIENNNSGWKVSLNYGEIIWTLQDNKQNIQRVVFKYSQMVNISDYINRWFV 1017

Query: 181 ITNN-LNNAKIYINGKLESNTDIKDIRREVIANGEIIFKLDGDIDRTQFIFWMKYFSIFNTE 239
 ITNN L +KIVYNG+L I ++ + A+ +T+FKLIDG D ++I +KYF+F+ E

Sbjct: 1018 ITNNRLTKSKIYINGRLIDQKPIISNLGNIHASNKIMFKLDGCRDPRRYIMIKYFNLFDKE 1077

Query: 240 LSQSNEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNYSYIKLKK-----DS 290
L++ I++ Y QS S LKDFWGN L Y+K YYM N + N Y+ +

Sbjct: 1078 LNEKEIKDLYDSQNSNSGILKDFWGNYLQYDKPYYMLNLFPNKYVDVNNIGIRGYMYLKG 1137

Query: 291 PVGEILTRSKYNQNSKYINYRDLYIGEKFIIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQ 350
P G ++T + Y ++ LY G KFII++ ++ D+IVR D +Y++ N+

Sbjct: 1138 PRGSVVTNIYLNST-----LYEGTKFIKKYASGN--EDNIVRNNDRVYINVVKNK 1188

Query: 351 EWRVYXXXXXXXXXXXXXAPISDSDEFYNTIQIKEYDEQPTYSQOLLFKKDEESTDEIG 410
E+R+ T I D + +K D+Q + + +D D TG

Sbjct: 1189 EYRLATNASQAGVEKILSALEIPDVGNLSQLVVVMKSDDQGIRNKCKMNLQDNNGND-IG 1247

Query: 411 LIGIHRFYESGIVFEELYKDYFCISKWYLKEVKRKPYNLKGNCNWQFIPKDEGWTE 465
IG H + + S WY ++V + + GC+W+FLP D+GW E

Sbjct: 1248 FIGFHL-----DNIAKLVASNWYNRQVGKA--SRTFGCSWEFIPVDDGWGE 1292

tr Q58GH1 Type A2 botulinum neurotoxin [Clostridium botulinum] 1296 AA
Q58GH1_CLOBO

align

Score = 297 bits (761), Expect = 3e-79
Identities = 175/475 (36%), Positives = 259/475 (53%), Gaps = 35/475 (7%)

Query: 3 NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXXRYKDNNLIDLSGYGAKVEVY 62
N L +PF LS Y ++ L+ F +Y YK ++LIDLS YGAK+ +
Sbjct: 842 NNLSADIPEQLSKYVDNKKLLSTFTYEIKNIVNTSILSIVYKKDDLIDLSRYGAKINIG 901

Query: 63 DGVELN--DKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVFWIRIPKYKNDGIQNYI 120
D V + DKNQ KL + +S I V I+NS++ +FS SFWI+IPKY + + +
Sbjct: 902 DRVYYDSIDKNQIKLINLESSTIEVILKNAIVYNSMYENFSTSFWIKIPKYFS---KINL 958

Query: 121 HNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVT 180
+NEYTIINC++NNSGWK+S+ IIWTL D + V F+Y+ +IS+YINRW FVT
Sbjct: 959 NNEYTIINCIENNNSGWKVSINYGEIIIWTLQDNKQNIQRVVFKYSQMVNISDYINRWIFVT 1018

Query: 181 ITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTE 239
ITNN L +KIYING+L I ++ +A+ +I+FKLDG D ++I +KYF++F+ E
Sbjct: 1019 ITNNRLTKSKIYINGRLIDQKPIISNLGNIHASNKIMFKLDGCRDPRRYIMIKYFNLFDKE 1078

Query: 240 LSQSNEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNYSYIKLKK-----DS 290
L++ I++ Y QS S LKDFWGN L Y+K YYM N + N Y+ +

Sbjct: 1079 LNEKEIKDLYDSQNSNSGILKDFWGNYLQYDKPYYMLNLFPNKYVDVNNIGIRGYMYLKG 1138

Query: 291 PVGEILTRSKYNQNSKYINYRDLYIGEKFIIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQ 350
P G ++T + Y ++ LY G KFII++ ++ D+IVR D +Y++ N+

Sbjct: 1139 PRGSVVTNIYLNST-----LYEGTKFIKKYASGN--EDNIVRNNDRVYINVVKNK 1189

Query: 351 EWRVYXXXXXXXXXXXXXAPISDSDEFYNTIQIKEYDEQPTYSQOLLFKKDEESTDEIG 410
E+R+ T I D + +K D+Q + + +D D TG

Sbjct: 1190 EYRLATNASQAGVEKILSALEIPDVGNLSQLVVVMKSDDQGIRNKCKMNLQDNNGND-IG 1248

Query: 411 LIGIHRFYESGIVFEELYKDYFCISKWYLKEVKRKPYNLKGNCNWQFIPKDEGWTE 465
IG H + + S WY ++V + + GC+W+FLP D+GW E

Sbjct: 1018 ITNNRLTKSKIYINGRLIDQKPIISNLGNIHASNKIMFKLDGCRDPRRYIMIKYFNLFDKE 1077

Query: 240 LSQSNEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKK-----DS 290
L++ I++ Y QS S LKDFWGN L Y+K YYM N + N Y+ +

Sbjct: 1078 LNEKEIKDLYDSQNSNSGILKDFWGNYLQYDKPYYMLNLFPNKYVDVNNIGIRGYMYLKG 1137

Query: 291 PVGEILTRSKYNQNSKYINYRDLYIGEKFIIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQ 350
P G ++T + Y ++ LY G KFII++ ++ D+IVR D +Y++ N+

Sbjct: 1138 PRGSVVTTNIYLNST-----LYEGTKFIKKYASGN--EDNIVRNNDRVYINVVKNK 1188

Query: 351 EWRVYXXXXXXXXXXXXXAPISDSDEFYNTIQIKEYDEQPTYSQQLFKKDEESTDEIG 410
E+R+ T I D + +K D+Q + + +D D TG

Sbjct: 1189 EYRLATNASQAGVEKILSALEIPDVGNLSQLVVVMSKDDQGIRNKCKMNLQDNNGND-IG 1247

Query: 411 LIGIHRFYESGIVFEELYKDYFCISKWYLKEVKRKPYNLKGNCNWQFIPKDEGWTE 465
IG H + + S WY ++V + + GC+W+FIP D+GW E

Sbjct: 1248 FIGFHL-----DNIAKLVASNWYNRQVGKA--SRTFGCSWEFIPVDDGWGE 1292

tr Q58GH1 Type A2 botulinum neurotoxin [Clostridium botulinum] 1296 AA
Q58GH1_CLOBO

align

Score = 297 bits (761), Expect = 3e-79
Identities = 175/475 (36%), Positives = 259/475 (53%), Gaps = 35/475 (7%)

Query: 3 NKYLKTIMPFDLSIYTNDTILIEFMNKYNSEXXXXXXXXXXRYKDNNLIDLSGYGAKVEVY 62
N L +PF LS Y ++ L+ F +Y YK ++LTDSL YGAK+ +

Sbjct: 842 NNTLSADIPFQLSKYVDNKKLLSTFTEYIKNIVNTSILSIVYKKDDLIDLSRYGAKINIG 901

Query: 63 DGVELN--DKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFIRIPKYKNDGIQNYI 120
D V + DKNQ KL + +S I V I++NS++ +FS SFWI+IPKY + + +

Sbjct: 902 DRVYYDSIDKNQIKLINLESSTIEVILKNAIVYNSMYENFSTSFWIKIPKYFS---KINL 958

Query: 121 HNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVT 180
+NEYTIINC++NNSGWK+S+ IIWTI D + V F+Y+ +IS+YINRW FVT

Sbjct: 959 NNEYTIINCIENNNSGWKVSLNYGEIIWTLQDNKQNIQRVVFKYSQMVNISDYINRWIFVT 1018

Query: 181 ITNN-LNNAKIYINGKLESNTDIKDIRREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTE 239
ITNN L +KIYING+L I ++ + A+ +I+FKLDG D ++I +KYF++F+ E

Sbjct: 1019 ITNNRLTKSKIYINGRLIDQKPIISNLGNIHASNKIMFKLDGCRDPRRYIMIKYFNLFDKE 1078

Query: 240 LSQSNEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKK-----DS 290
L++ I++ Y QS S LKDFWGN L Y+K YYM N + N Y+ +

Sbjct: 1079 LNEKEIKDLYDSQNSNSGILKDFWGNYLQYDKPYYMLNLFPNKYVDVNNIGIRGYMYLKG 1138

Query: 291 PVGEILTRSKYNQNSKYINYRDLYIGEKFIIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQ 350
P G ++T + Y ++ LY G KFII++ ++ D+IVR D +Y++ N+

Sbjct: 1139 PRGSVVTTNIYLNST-----LYEGTKFIKKYASGN--EDNIVRNNDRVYINVVKNK 1189

Query: 351 EWRVYXXXXXXXXXXXXXAPISDSDEFYNTIQIKEYDEQPTYSQQLFKKDEESTDEIG 410
E+R+ T I D + +K D+Q + + +D D TG

Sbjct: 1190 EYRLATNASQAGVEKILSALEIPDVGNLSQLVVVMSKDDQGIRNKCKMNLQDNNGND-IG 1248

Query: 411 LIGIHRFYESGIVFEELYKDYFCISKWYLKEVKRKPYNLKGNCNWQFIPKDEGWTE 465
IG H + + S WY ++V + + GC+W+FIP D+GW E

Sbjct: 1249 FIGFHLY-----DNIAKLVASNWYNRQVGKA--SRTFGCSWEFIPVDDGWGE 1293

tr [Q9ZAJ5](#) **BonT protein [bonT] [Clostridium botulinum]** 1280 AA
[Q9ZAJ5_CLOBO](#)

Score = 281 bits (720), Expect = 2e-74
 Identities = 172/469 (36%), Positives = 255/469 (53%), Gaps = 35/469 (7%)

Query: 6 LKTIMPFDLSIYTNDTILIEFMNKYNSEXXXXXXXXRYKDNNLIDLSGYGAKVEVYDGV 65
 L + +PF+LS YTND ILT FN+ + RY++N TD+SGYG+ + + V

Sbjct: 838 LNNSIPFELSSYTNDKILIIYFNRLYKKIKDSSILDMDRYENNKFIDISGYGSNISINGNV 897

Query: 66 EL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWRIPKYKNDGIQNYIHNE 123
 + +NQF + S S++ + QN +II+NS + +FS+SFW+ RIPK+ +N E

Sbjct: 898 YIYSTNRNQFGIYSGRLSEVNIAQNNDIYNSRYQNFISFWVTIPKHYRPMNRN--RE 954

Query: 124 YTIINCM-KNNSGWKISIRGNR--IIWTLIDINGKTKSVFFEYNIREDISEYINRWFFV 179

YTIINCM NNSGWKIS+R R LIWTL D +G + + F Y IS+YIN+W EV

Sbjct: 955 YTIINCMGNNSGWKISLRTIRDCEIIWTLQDTSGNKEKLIFYEEELASISDYINKWIFV 1014

Query: 180 TITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNT 238
 TITNN I N++IYING L I + + + + I+EK+ G D T + + + +YF +FNT

Sbjct: 1015 TITNNRLGNSRIYINGNLIVEKSISNLGDIHVSNDNILFKIVGCDDET-YVGIRYFKVFNT 1073

Query: 239 ELSQSNEERYKIQSYSEYLKDFWGNPLMYNKEYMFNAGNKNSYIKLKKDSPVGEI-LT 297
 EL: ++ TE Y + LKD+WGN L+YNK+YY+FN K+ YI ++S + I

Sbjct: 1074 ELDKTEIETLYSNEPDPSILKDYWGNYLLYNKKYYLFNLLRKDKYI--TRNSGILNINQQ 1131

Query: 298 RSKYNQNSKYINYRDLYIGEKFIIIRRKSNSQ SIN-DDIVRKEDYIYLDFFNLNQEWRVYT 356
 R S + +NY+ LY G + IER+ + N D+ VRK D Y++ + E+R+Y

Sbjct: 1132 RGVTGGISVFLNYK-LYEGVEVIIRKNAPIDISNTDNFVRKNDLAYINVVDHGVEYRLYA 1190

Query: 357 XXXXXXXXXXXXAPISDSDEFYNTIQIKEKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHR 416
 S+ ++ I + + + C + F+ ++ S IGL+G R

Sbjct: 1191 DISITKSEKIIKLIRTSNPNDSLGQIIVM--DSIGNNCTMFQNNDGS--NIGLLGFH- 1244

Query: 417 FYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLCNWQFIPKDEGWTE 465

D S WY ++R . GC W FI K+ GW E

Sbjct: 1245 -----SDDLVASSWYYNHIRRN--TSSNGCFWSFISKEHWKE 1280

tr [Q57236](#) **BoNT/F (Neurotoxin type F) [bont/f] [Clostridium botulinum]** 1278 AA
[Q57236_CLOBO](#)

Score = 281 bits (718), Expect = 3e-74
 Identities = 166/465 (35%), Positives = 254/465 (53%), Gaps = 30/465 (6%)

Query: 6 LKTIMPFDLSIYTNDTILIEFMNKYNSEXXXXXXXXRYKDNNLIDLSGYGAKVEVYDGV 65
 L + +PF+LS YTND ILT FNK + RY++N TD+SGYG+ + + V

Sbjct: 838 LNNSIPFELSSYTNDKILILYFNKLYKKIKDSSILDMDRYENNKFIDISGYGSNISINGDV 897

Query: 66 EL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWRIPKYKNDGIQNYIHNE 123
 + +NQF + SS S++ + QN +II+N + +FS+SFW+RIPKY N + +NE

Sbjct: 1249 FIGFHLY-----DNIAKLVASNWYNRQVGKA--SRTFGCSWEFIPVDDGWGE 1293

tr Q9ZAJ5 **BonT protein [bonT] [Clostridium botulinum]** 1280 AA
Q9ZAJ5_CLOBO

Score = 281 bits (720), Expect = 2e-74
 Identities = 172/469 (36%), Positives = 255/469 (53%), Gaps = 35/469 (7%)

Query: 6 LKТИMPFDLSIYTNDTILIEFNKYNSEXXXXXXXXRYKDNNLIDLSGYGAKVEVYDGV 65
 L + +PF+LS YTNND ILT FNK + RY++N ID+SGYG+ + + V

Sbjct: 838 LNNSIPFELSSYTNDKILIIYFNRLYKKIKDSSILDMDRYENNKFIDISGYGSNISINGNV 897

Query: 66 EL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLLDFSVSFWRIPKYKNDGIQNYIHNE 123
 + + +NQF + S S++ + QN +II+NS + +FS+SFW+ IPK+ +N E

Sbjct: 898 YIYSTNRNQFGIYSGRLSEVNIAQNNDIYNSRYQNFSISFWVTIPKHYRPMNRN---RE 954

Query: 124 YTIIINCM-KNNSGWKISIRGNR---IIWTLIDINGKTKSVFFEYNIREDISEYINRWFFV 179
 YTIIINCM NNSGWKIS+R R IEWTL D +G + + F Y IS+YIN+W FV

Sbjct: 955 YTIIINCMGNNSGKISLRTIRDCEIIWTLQDTSGNKEKLIFYEEELASISDYINKWIFV 1014

Query: 180 TITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNT 238
 TITNN I. N++IYING L . I + + + + I+EK+ G D T + + + +YF +FNT

Sbjct: 1015 TITNNRLGNSRIYINGNLIVEKSISNLGDIHVSNDNILFKIVGCDDET-YVGIRYFKVFNT 1073

Query: 239 ELSQSNIIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEI-LT 297
 EJ. ++ IE Y + IED+WGQ I+YNK+YY+FN K+ YI + +S + T

Sbjct: 1074 ELDKTEIETLYSPDPSILKDYWGNYLLYNKYYLFNLLRKDKYI--TRNSGILNINQQ 1131

Query: 298 RSKYNQNSKYINYRDLYIGEKFIIIRKSNQSIN-DDIVRKEDYIYLDFFNLNQEWRVYT 356
 R S ++NY+ LY G + IIR+ + N D+ VRK D Y++ + E+R+Y

Sbjct: 1132 RGVTGGISVFLNYK-LYEGVEVIIRKNAPIDISNTDNFVRKNDLAYINVVDHGVEYRLYA 1190

Query: 357 XXXXXXXXXXXXAPISDSDEFYNTIQIKEYDEQPTYSQQLFFKKDEESTDEIGLIGIHR 416
 S+ ++ I + + + +C + F+ ++ S IGL+G R

Sbjct: 1191 DISITKSEKIIKLIRTSNPNDLQIIVM---DSIGNNCTMNFQNNDG--NIGLLGFH- 1244

Query: 417 FYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLCNWQFIPKDEGWTE 465
 D S WY ++R GC W FI K+ GW E

Sbjct: 1245 -----SDDLVASSWYYNHIRRN--TSSNGCFWSFISKEHWKE 1280

tr Q57236 **BoNT/F (Neurotoxin type F) [bont/f] [Clostridium botulinum]** 1278
Q57236_CLOBO AA
align

Score = 281 bits (718), Expect = 3e-74
 Identities = 166/465 (35%), Positives = 254/465 (53%), Gaps = 30/465 (6%)

Query: 6 LKТИMPFDLSIYTNDTILIEFNKYNSEXXXXXXXXRYKDNNLIDLSGYGAKVEVYDGV 65
 L + +PF+LS YTNND ILT FNK + RY++N ID+SGYG+ + + V

Sbjct: 838 LNNSIPFELSSYTNDKILILYFNKLYKKIKDSSILDMDRYENNKFIDISGYGSNISINGDV 897

Query: 66 EL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLLDFSVSFWRIPKYKNDGIQNYIHNE 123
 + + +NQF + SS S++ + QN +II+N + +FS+SFW+IPK Y N + + +NE

Sbjct: 898 YIYSTNRNQFGIYSSKPSEVNIAQNNDDIIYNGRYQNFSISFWVRIPKYFN---KVNLNNE 954

Query: 124 YTIIINCMKNN-SGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTIT 182
YTII+C++NN SGWKIS+ N+IIWTL D G + + F Y IS+YIN+W FVTIT

Sbjct: 955 YTIIDCIRNNNSGWKISLNLYNKKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTIT 1014

Query: 183 NN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDDIDRTQFIWMKYFSIFNTELS 241
NN L N++IYING L I ++ + + I+FK+ G D T++ + +YF +F+TEL

Sbjct: 1015 NNRLGNSRIYINGNLIDEKSISNLGDIHVSNDNILFKIVGCND-TRYVGIRYFKVFDTELG 1073

Query: 242 QSNIEERYKIQSSEYLKDFWGNPLMYNKEYMFNAGNKNYSIKLKKDSPVGEILTRSKY 301
++ IE Y + LKDFWGN L+YNK YY+ N + I + + + R X

Sbjct: 1074 KTEIETLYSDEPDPSILKDFWGNYLLYNKRYLLNLLRTDKSI-TQNSNFLNINQQRGVY 1132

Query: 302 NQNSKYINYRDLYIGEKFIIRRKSNSQSIN-DDIVRKEDYIYLDFFNLNQEWRVYXXXX 360
+ + + N R LY G + IIR+ ++ N D+ VRE D Y++ + + E+R+Y

Sbjct: 1133 QKPNIFSNTR-LYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISI 1191

Query: 361 XXXXXXXXXXXXAPISDSDEFYNTIQIKEYDEQPTYSQQLFKKDEESTDEIGLIGIHRFYES 420
S+S+ I + + + C + F+ + + IGL+G H

Sbjct: 1192 AKPEKIKLIRTSNSNNSLGQIIVM--DSIGNCTMFQNN--NGGNIGLLGFH---- 1241

Query: 421 GIVFEEYKDYFCISKWYLKEVKRKPYNLKGNCNWQFIPKDEGWTE 465
+ S WY + + + GC W FI K+ GW E

Sbjct: 1242 -----SNNLVASSWYYNNIRKN--TSSNGCFWSFISKEHWQE 1277

sp <u>P30996</u>	Botulinum neurotoxin type F precursor (EC 3.4.24.69)	1274
BXF_CLOBO	(BoNT/F)	AA
	(Bontoxilysin F) [botF] [Clostridium botulinum]	<u>align</u>

Score = 278 bits (712), Expect = 1e-73
Identities = 171/474 (36%), Positives = 255/474 (53%), Gaps = 50/474 (10%)

Query: 6 LKTIMPFDLSIYTNDTILIMFNKYNSEXXXXXXXXRYKDNNLIDLGYGAKVEVYDGV 65
L + +PF+LS YTND ILI FN+ + RY++N ID+SGYG+ + + V

Sbjct: 837 LNSSIPFELSSYTNDKILIYFNRLYKKIKDSSILDMDRYENNKFIDISGYGSNISINGNV 896

Query: 66 EL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWRIPKYKNDGIQNYIHNE 123
+ +NQF + +S S++ + QN +LI+NS + +FS+SEW+RIPK+ N E

Sbjct: 897 YIYSTNRNQFGIYNSRLSEVNIAQNNDDIIYNSRYQNFSISFWVRIPKHYKPMNHN--RE 953

Query: 124 YTIIINCM-KNNSGWKISIRGNR--IIWTLIDINGKTKSVFFEYNIREDISEYINRWFFV 179
YTIIINCM NNNGWKIS+R R IIWTL D +G + + F Y IS YIN+W FV

Sbjct: 954 YTIIINCMGNNSGWKISLRTVRDCEIIWTLQDTSGNKENLIFRYEELNRISNYINKWIFV 1013

Query: 180 TITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDDIDRTQFIWMKYFSIFNT 238
TITNN L N++IYING L I ++ + + I+FK+ G D T ++ + +YF +FNT

Sbjct: 1014 TITNNRLGNSRIYINGNLIVEKSISNLGDIHVSNDNILFKIVGCDDET-YVGIRYFKFNT 1072

Query: 239 ELSQSNEERYKIQSSEYLKDFWGNPLMYNKEYMFNAGNKNYSIKLKKDSPVGEILTR 298
EL ++ IE Y + LK++WGN L+YNK+YY+FN K+ YI L +S + I +

Sbjct: 1073 ELDKTEIETLYSNEPDPSILKNYWGNYLLYNKYYLFNLLRKDKYITL--NSGILNINQQ 1130

Query: 299 SKYNQNSKYINYRDLYIGEKFIIRRKSNSQSIN-DDIVRKEDYIYLDFFNLNQEWRVYTX 357
+ S + +NY+ LY G + IIR+ N D+ VRK D Y++ + E+R+Y

Sbjct: 898 YIYSTNRNQFGIYSSKPSEVNIAQNNDDIIYNGRYQNFISFWVRIPKYFN---KVNLNNE 954

Query: 124 YTIIINCMKNN-SGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTIT 182
YTII+C++NN SGWKIS+ N+IWTL D G + + F Y IS+YIN+W FVTIT

Sbjct: 955 YTIIDCIRNNNSGWKISLNLYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTIT 1014

Query: 183 NN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGIDRTQFIWMKYFSIFNTELS 241
NN L N++IYING L I ++ + + I+FK+ G D T+++ ++YF +F+TEL

Sbjct: 1015 NNRLGNSRIYINGNLIDEKSISNLGDIHVSNDILFKIVGCND-TRYVGIRYFKVFDTELG 1073

Query: 242 QSNIEERYKIQSSEYLKDFWGNPLMYNKEYYMFNAGNKNYSIKLKKDSPVGEILTRSKY 301
++ IE Y + LKDWGN L+YNK YY+ N + I + + + R X

Sbjct: 1074 KTEIETLYSDEPDPSILKDFWGNYLLYNKRYLLNLLRTDKSI-TQNSNFLNINQQRGVY 1132

Query: 302 NQNSKYINYRDLYIGEKFIIRRKSNSQSIN-DDIVRKEDYIYLDFFNLNQEWRVYXXXX 360
+ + + N R LY G + IER+ ++ N D+ VRK D Y++ + + E+R+Y

Sbjct: 1133 QKPNIFSNTR-LYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISI 1191

Query: 361 XXXXXXXXXXXXAPISDSDEFYNTIQIKEYDEQPTYSQOLLFKKDEESTDEIGLIGIHRFYES 420
S+S+ I + + + C + F+ + + IGL+G H

Sbjct: 1192 AKPEKIKLIRTSNSNNSLGQIIVM--DSIGNCTMFQNN--NGGNIGLLGFH----- 1241

Query: 421 GIVFEEYKDYFCISKWYLKEVKRKPYNLKGNCNWQFIPKDEGWTE 465
+ S WY +++ GC W FI K+ GW E

Sbjct: 1242 -----SNNLVASSWYNNIRKN--TSSNGCFWSFISKEHWQE 1277

sp	<u>P30996</u>	Botulinum neurotoxin type F precursor (EC 3.4.24.69)	1274
BXF_CLOBO	(BoNT/F)	AA	
	(Bontoxilysin F) [botF] [Clostridium botulinum]	<u>align</u>	

Score = 278 bits (712), Expect = 1e-73
 Identities = 171/474 (36%), Positives = 255/474 (53%), Gaps = 50/474 (10%)

Query: 6 LKTIMPFDLSIYTNDTILIMFNKYNSEXXXXXXXXRYKDNNLIDLGYAKVEVYDGV 65
L + +PF+LS YTND ELI FN+ + RY++N ID+SGYG+ + + V

Sbjct: 837 LNSSIPFELSSYTNDKILIIYFNRLYKKIKDSSILDMDRYENNKFIDISGYGSNISINGNV 896

Query: 66 EL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSEWIRIPKYKNDGIQNYIHNE 123
+ + +NQF + +S S++ + QN +II+NS + +FS+SFW+RIPK+ N E

Sbjct: 897 YIYSTNRNQFGIYNSRLSEVNIAQNNDDIIYNSRYQNFISFWVRIPKHYKPMNHN--RE 953

Query: 124 YTIIINCM-KNNSGWKISIRGNR--IIWTLIDINGKTKSVFFEYNIREDISEYINRWFFV 179
YTIIINCM NNNSGWKIS+R R IWTL D +G + + F Y IS YIN+W FV

Sbjct: 954 YTIIINCMGNNSGWKISLRTVRDCEIIWTLQDTSGNKENLIFYEELNRISNYINKWIFV 1013

Query: 180 TITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGIDRTQFIWMKYFSIFNT 238
TITNN L N++IYING L I ++ + + I+FK+ G D T ++ ++YF +FNT

Sbjct: 1014 TITNNRLGNSRIYINGNLIVEKSISNLGDIHVSNDILFKIVGCDDET-YVGIRYFKVFT 1072

Query: 239 ELSQSNEERYKIQSSEYLKDFWGNPLMYNKEYYMFNAGNKNYSIKLKKDSPVGEILTR 298
EL ++ IE Y + LK++WGN L+YNK+YY+FN K+ YI L +S + I +

Sbjct: 1073 ELDKTEIETLYSNEPDPSILKNYWGNYLLYNKYYLFNLLRKDKYITL--NSGILNINQQ 1130

Query: 299 SKYNQNSKYINYRDLYIGEKFIIRRKSNSQSIN-DDIVRKEDYIYLDFFNLNQEWRVYTX 357
+ S ++NY+ LY G + IER+ N D+ VRK D Y++ + E+R+Y

Sbjct: 1131 RGVTEGSVFLNYK-LYEGVEVIIRKNGPIDISNTDNFVRKNDLAYINVVDRGVEYRLYAD 1189
 Query: 358 XXXXXXXXXXXXAPISDSDEFYNTIQIKEYDEQPTY-----SCQLLFKKDEESTDEIGL 411
 S+ ++ T + + Q +C + F+ + S IGL
 Sbjct: 1190 TK-----SEKEKIIRTSNLNDSLGQIIVMDSIGNNCTMFQNNNGS--NIGL 1234
 Query: 412 IGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE 465
 +G K + S WY +R GC W I K+ GW E
 Sbjct: 1235 LGFH-----SNNLVASSWYNNIRRN--TSSNGCFWSSISKENGWKE 1274

sp Q00496 Botulinum neurotoxin type E precursor (EC 3.4.24.69) 1250
 BXE_CLOBO (BoNT/E) AA
 (Bontoxilysin E) [Clostridium botulinum] align

Score = 273 bits (699), Expect = 4e-72
 Identities = 163/469 (34%), Positives = 250/469 (52%), Gaps = 36/469 (7%)

Query: 1 MANKYLKTIMPFDLSIYTNDTILIEFMNKYNSEXXXXXXXXXRYKDNNNLIDLSGYGAKVE 60
 M L +PF LS YT+D ILL ENK+ SYK++ +D SGY + +
 Sbjct: 813 MVTDTLNNSIPFKLSSYTDDKILISYFNKFFKRIKSSSVLMRKYKNDKYVDTSGYDSNIN 872

Query: 61 VYDGVEL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFIRIPKYKNDGIQN 118
 + V +KNQF + + S++ +QN II+++ + +FS+SFW+RIP Y N +
 Sbjct: 873 INGDVYKYPTNKNQFGIYNDKLSEVNISQNDIYIYDNKYKNFSISFWVRIPNYDNKIVN- 931

Query: 119 YIHNEYTIINCMK-NNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWF 177
 + +NEYTIINCM+ NNSGWK+S+ N LIWT D G + + F Y IS+YIN+W
 Sbjct: 932 -VNNEYTIINCMRDNNSGWKVSLNHNEIIWTFEDNRGINQKLAFLNYGNANGISDYINKWI 990

Query: 178 FVTITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIF 236
 FVTITNN+ L + +K+YING L I ++ + + I+ENK+ + T++I + +YF+IF
 Sbjct: 991 FVTITNDRLGDSKLYINGNLIDQKSILNLGNIHVDNILFKIV-NCSYTRYIGIRYFNIF 1049

Query: 237 NTELSQSNEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEIL 296
 + EL ++ I+ Y + + LKDFWGN L+Y+KEYY+ N N+I +KDS
 Sbjct: 1050 DKELDETEIQTLYSNEPNTNLKDFWGNYLKYDKEYYLLNVLPNNFIDRRKDS----- 1103

Query: 297 TRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYT 356
 T S N S + LY G K I+F +NS S ND++VRA D +Y++F + + +
 Sbjct: 1104 TLSINNIRSTILLANRLYSGIKVKIQRVNNS-STNDNLVRKNDQVYINF--VASKTHLFP 1160

Query: 357 XXXXXXXXXXXXAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHR 416
 IS S +N + + +C + FK + + + IGL+G
 Sbjct: 1161 LYADTATTNKEKTIKISSSGNRFNQVVVM---NSVGNCNFKN--NGNNIGLLGFK- 1213

Query: 417 FYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE 465
 D S WY + + + GC W FI ++ GW E
 Sbjct: 1214 -----ADTVVASTWYTHM--RDHTNSNGCFWNFISEEHGWQE 1249

tr Q9K395 Type E botulinum toxin [bont/E] [Clostridium butyricum] 1251 AA
Q9K395_CLOBU align

Sbjct: 1131 RGVTEGSVFLNYK-LYEGVEVIIRKNGPIDISNTDNFVRKNDLAYINVVDRGVEYRLYAD 1189

Query: 358 XXXXXXXXXXXXAPISDSDEFYNTIQIKEYDEQPTY----SCQLLFKKDEESTDEIGL 411
S+ ++ T + + Q +C + F+ + S IGL

Sbjct: 1190 TK-----SEKEKIIRTSNLNSLGQIVMDSIGNNCTMNFQNNNGS--NIGL 1234

Query: 412 IGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLCNWQFIPKDEGWTE 465
+G K + S WY ++R GC W I K+ GW E

Sbjct: 1235 LGFH-----SNNLVASSWYNNIRRN--TSSNGCFWSSISKENGWKE 1274

sp Q00496 Botulinum neurotoxin type E precursor (EC 3.4.24.69) 1250
BXE_CLOBO (BoNT/E) AA
(Bontoxilysin E) [Clostridium botulinum] align

Score = 273 bits (699), Expect = 4e-72

Identities = 163/469 (34%), Positives = 250/469 (52%), Gaps = 36/469 (7%)

Query: 1 MANKYLKTIMPFDLSIYTNDTILIEFMNKYNSEXXXXXXXXXRYKDNNLIDLSGYGAKVE 60
M L +PF LS YT+D ILL FNK+ SYK++ +D SGY + +

Sbjct: 813 MVTDTLNNSIPFKLSSYTDDKILISYFNKFFKRIKSSSVLMRKYKNDKYVDTSGYDSNIN 872

Query: 61 VYDGVEL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWRIPKYKNDGIQN 118
+ V +KNQF + + S++ ++QN TI+++ + +FS+SFW+RIP Y N +

Sbjct: 873 INGDVYKYPTNKNQFGIYNDKLSEVNISQNDYIIYDNKYKNFSISFWVRIPNYDNKIVN- 931

Query: 119 YIHNEYTIINCMK-NNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWF 177
++NEYTIINCM+ NNSGWK+S+ N IIWT D G + + F Y IS+YIN+W

Sbjct: 932 -VNNEYTIINCMRDNNSGWKVSLNHNEIIWTFEDNRGINQKLAFTNANGISDYINKWI 990

Query: 178 FVTITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIF 236
FVTITNN+ L ++K+YING L T ++ + + T+FK+ + T++I ++YF+IE

Sbjct: 991 FVTITNDRLGDSKLYINGNLIDQKSILNLGNIHVDNILFKIV-NCSYTRYIGIRYFNIF 1049

Query: 237 NTELSQSNIEERYKIQSYSEYLKDFWGPNPLMYNKEYMFNAGNKNYSIKLKKDSPVGEIL 296
+ RL ++ I+ Y + + LKDFWGK L+Y+KEYY+ N N++I +KDS

Sbjct: 1050 DKELDETEIQTLYSNEPNTNLKDFWGNLYDKEYYLLNVLPNNFIDRRKDS----- 1103

Query: 297 TRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYT 356
T S N S + LY G K I+R +NS S ND++VRK D +Y++F + + ++

Sbjct: 1104 TLSINNIRSTILLANRLYSGIKVKIQRVNNS-STNDNLVRKNDQVYINF--VASKTHLFP 1160

Query: 357 XXXXXXXXXXXXAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHR 416
IS S +N + + +C + FK + + + IGL+G

Sbjct: 1161 LYADTATTNKEKTIKISSSGNRFNQVVVM---NSVGNCNMFKNN--NGNNIGLLGFK- 1213

Query: 417 FYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLCNWQFIPKDEGWTE 465

D S WY + + + GC W FI ++ GW E

Sbjct: 1214 -----ADTVVASTWYTHM--RDHTNSNGCFWNFISEEHGWQE 1249

tr Q9K395 Type E botulinum toxin [bont/E] [Clostridium butyricum] 1251 AA
Q9K395_CLOBU

align

Score = 267 bits (683), Expect = 3e-70
 Identities = 159/464 (34%), Positives = 247/464 (52%), Gaps = 36/464 (7%)

Query: 6 LKTIMPFDLSIYTNDTILIEFMNKYNSEXXXXXXXXXRYKDNNLIDLSGYGAKVEVYDGV 65
 Sbjct: 819 LNN SIPFKLSSYTDDKILIS YFNKFFKRIKSSSVLMRKYKNDKYVDTSGYDSNININGEI 878

Query: 66 EL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFDFSVSFWIRIPKYKNDGIQNYIHNE 123
 Sbjct: 879 FIYPTNKNQFTIFNSKPSEVNISQNDYIIYDNKYKNFSISFWVRIPNYDNKIVN--INNE 936

Query: 124 YTIINCMK-NNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTIT 182
 Sbjct: 937 YTIINCMRDNNSGWKVSLNHNEIIWTLQDNARINQKLVFKYGNANGISDYINKWIFVTIT 996

Query: 183 NN-LNNAKIYINGKLESNTDIKDIREVIANGEIIIFKLDGDIDRTQFIFIWMKYFSIFNTELS 241
 Sbjct: 997 NDRLGDSKLYINGHLIDQKSILNLGNIHVDNILFKIV-NCSYTRYIGIRYFNIFDKELD 1055

Query: 242 QSNIEERYKIQSSEYLKDFWGPNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKY 301
 Sbjct: 1056 ETEIQTLYSNEPNTNILKDFWGNYLLYDKGYYLLNVLKPNNFIDRRKDS-----TLSIN 1109

Query: 302 NQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFNLNQEWRVYXXXXX 361
 Sbjct: 1110 NIRSTILLANRLYSGIKVKIQR-VNDSSTNDRFVRKNDQVYINYISNSSSYSLYADTTT 1168

Query: 362 XXXXXXXXAPISDSDEFYNTIQIKEYDEOPTYSCQLLFKKDEESTDEIGLIGIHRFYESG 421
 Sbjct: 1169 DKEKTIKSS--SSGNRFNQVVMNSVGN---NCTMNFKNN--NGNNIGLLGFK----- 1214

Query: 422 IVFEEYKDYFCISKWYLKEVKRKPYNLKGNCNWQFIPKDEGWTE 465
 Sbjct: 1215 -----ADTVVASTWYYTHM--RDHTNSNGCFWNFISEEHGWQE 1250

sp P30995 Botulinum neurotoxin type E precursor (EC 3.4.24.69) 1250
 BXE_CLOBU (BoNT/E) AA
 (Bontoxilysin E) [Clostridium butyricum] align

Score = 266 bits (680), Expect = 7e-70
 Identities = 161/464 (34%), Positives = 248/464 (52%), Gaps = 36/464 (7%)

Query: 6 LKTIMPFDLSIYTNDTILIEFMNKYNSEXXXXXXXXXRYKDNNLIDLSGYGAKVEVYDGV 65
 Sbjct: 818 LNN SIPFKLSSYTDDKILIS YFNKFFKRIKSSSVLMRKYKNDKYVDTSGYDSNININGDV 877

Query: 66 EL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFDFSVSFWIRIPKYKNDGIQNYIHNE 123
 Sbjct: 878 YKYPTNKNQFGIYNDKLSEVNISQNDYIIYDNKYKNFSISFWVRIPNYDNKIVN--VNNE 935

Query: 124 YTIINCMK-NNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTIT 182
 Sbjct: 936 YTIINCMRDNNSGWKVSLNHNEIIWTLQDNNSGINQKLAFNYGNANGISDYINKWIFVTIT 995

Query: 183 NN-LNNAKIYINGKLESNTDIKDIREVIANGEIIIFKLDGDIDRTQFIFIWMKYFSIFNTELS 241

Score = 267 bits (683), Expect = 3e-70
 Identities = 159/464 (34%), Positives = 247/464 (52%), Gaps = 36/464 (7%)

Query: 6 LKTIMPFDLSIYTNDTILIEFMNKYNSEXXXXXXXXXRYKDNNLIDLSGYGAKVEVYDGV 65
 L +PF LS YT+D ILI FNK+ RYK++ +D SGY + + + +
 Sbjct: 819 LNNSIPFKLSSYTDDKILISYFNKFFKRIKSSSVLNMRKYKNDKYVDTSGYDSNININGEI 878

Query: 66 EL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWRIPKYKNDGIQNYIHNE 123
 + +KNQF + +S S++ ++QN TT+++ + +FS+SFW+RIP Y N + I+NE
 Sbjct: 879 FIYPTNKNQFTIFNSKPSEVNISQNDIYIDNKYKNFSISFWVRIPNYDNKIVN--INNE 936

Query: 124 YTIINCMK-NNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTIT 182
 YTIINCM+ NNSGWK+S+ N IIWTL D + + F+Y IS+YIN+W FVTIT
 Sbjct: 937 YTIINCMRDNNSGWKVSLNHNIEIIWTLQDNARINQKLVFKYGNANGISDYINKWIFVTIT 996

Query: 183 NN-LNNAKIYINGKLESNTDIKDIREVIANGEIIIFKLDGDIDRTQFIWMKYFSIFNTELS 241
 N+ L ++K+YING L I ++ + + F+EK+ + T++T ++YF+IWF+ EI
 Sbjct: 997 NDRLGDSKLYINGHLIDQKSILNLGNIHVSNDNLFKIV-NCSYTRYIGIRYFNIFDKELD 1055

Query: 242 QSNIEERYKIQSSEYLKDFWGPNPLMYNKEYYMFMAGNKNYSIKLKKDSPVGEILTRSKY 301
 ++ I+ Y + + IAKDFWGNI L+Y+K YY+N N+I +KDS T S
 Sbjct: 1056 ETEIQTLYSNEPNTNILKDFWGNYLLYDKGYYLLNVLKPNNFIDRRKDS-----TLSIN 1109

Query: 302 NQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFNLNQEWRVYXXXXX 361
 N S + LY G K I+R N S ND VRK D +Y++ + + + + Y
 Sbjct: 1110 NIRSTILLANRLYSGIKVKIQR-VNDSSTNDRFVRKNDQVYINYISNSSSYSLYADTTT 1168

Query: 362 XXXXXXXXAPISDSDEFYNTIQIKEYDEOPTYSCOLLFKKDEESTDEIGLIGIHRFYESG 421
 + S + F + + + C + FK + + + IGL+G
 Sbjct: 1169 DKEKTIKSS--SSGNRFNQVVVMNSVGN---NCTMNFKNN--NGNNIGLLGFK----- 1214

Query: 422 IVFEEYKDYFCISKWYLKEVKRKPYNLKGNCNWQFIPKDEGWTE 465
 D S WY + + + GC W FI ++ GW E
 Sbjct: 1215 -----ADTVVASTWYYTHM--RDHTNSNGCFWNFISEEHGWQE 1250

sp	<u>P30995</u>	Botulinum neurotoxin type E precursor (EC 3.4.24.69)	1250
BXE_CLOBU	(BoNT/E)		AA
	(Bontoxilysin E) [Clostridium butyricum]		<u>align</u>

Score = 266 bits (680), Expect = 7e-70
 Identities = 161/464 (34%), Positives = 248/464 (52%), Gaps = 36/464 (7%)

Query: 6 LKTIMPFDLSIYTNDTILIEFMNKYNSEXXXXXXXXXRYKDNNLIDLSGYGAKVEVYDGV 65
 L +PF LS YT+D ILI FNK+ RYK++ +D SGY + + + V
 Sbjct: 818 LNNSIPFKLSSYTDDKILISYFNKFFKRIKSSSVLNMRKYKNDKYVDTSGYDSNININGDV 877

Query: 66 EL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWRIPKYKNDGIQNYIHNE 123
 + +KNQF + + S++ ++QN II+++ + +FS+SFW+RIP Y N + ++NE
 Sbjct: 878 KYPTNKNQFGIYNDKLSEVNISQNDIYIDNKYKNFSISFWVRIPNYDNKIVN--VNNE 935

Query: 124 YTIINCMK-NNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTIT 182
 YTIINCM+ NNSGWK+S+ N IIWTL D +G + + F Y IS+YIN+W FVTIT
 Sbjct: 936 YTIINCMRDNNSGWKVSLNHNIEIIWTLQDNNSGINQKLAFNYGNANGISDYINKWIFVTIT 995

Query: 183 NN-LNNAKIYINGKLESNTDIKDIREVIANGEIIIFKLDGDIDRTQFIWMKYFSIFNTELS 241

N+ L ++K+YING L I ++ + + I+FK+ + T++I ++YF+IF+ EL
 Sbjct: 996 NDRLGDSKLYINGNLIDKKSILNLGNIHVDNILFKI-VNC SYTRYIGIRYFNIFDKELD 1054

 Query: 242 QSNIEERYKIQSSEYLKD FWGNPLM YNKEYY MFNAGN KNS YIKL KKDS PVGE ILTR SKY 301
 ++ I+ Y + + LKDFWGN L+Y+KEYY+ N N++I + DS T S
 Sbjct: 1055 ETEIQTLYNNEPNANILKDFWGNYLLYDKEYYLLNVLKPNNFINRRRTDS-----TLSIN 1108

 Query: 302 NQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRYTXXXXX 361
 N S + LY G K I+R +NS S ND++VRK D +Y++F + + +
 Sbjct: 1109 NIRSTILLANRLYSGIKVKIQRVNNS-STNDNLVRKNDQVYINF--VASKTHLLPLYADT 1165

 Query: 362 XXXXXXXXAPISDSDEFYNTIQIKEYDEQPTYS CQLLF KKDEESTDEIGLIGIHRFYESG 421
 IS S +N + + +C + FK + + + IGL+G
 Sbjct: 1166 ATTNKEKTIKISSSGNRFNQVVVM---NSVGNCTMNFKN--NGNNIGLLGFK----- 1213

 Query: 422 IVFEEYKDYFCISKWYLKEVKRKPYNLKG CNWQFIPKDEGWTE 465
 D S WY + + + G W F I ++ GW E
 Sbjct: 1214 -----ADTVVASTWYYTHMRDNTNS--NGFFWNFISEEHGWQE 1249

tr Q9FAR6 Type E botulinum toxin [bont/E] [Clostridium butyricum] 1255 AA
Q9FAR6 _CLOBU
align

Score = 266 bits (679), Expect = 9e-70
 Identities = 161/464 (34%), Positives = 248/464 (52%), Gaps = 35/464 (7%)

Query: 6 LKTIMPFDLSIYTNDTILIMFNKYNSEXXXXXXXXXRYKDNNLIDL SGY GAKVEYDGV 65
 L +PF LS YT+D XLI FNK+ RYK++ +D SGY + + + V
 Sbjct: 822 LNNSIPFKLSSYTDDKILISYFNKFFFRIKSSSVLMR YKNDKYVDTSGYDSNININGDV 881

 Query: 66 EL--NDKNQFKLTSSANSKIRVTQNQNI IFNSVFLDFS VSFWIRIPKYKNDGIQNYIHNE 123
 +KNQF + + S++ ++QN TI+++ + +FS+SFW+RIF Y N + ++NE
 Sbjct: 882 YKPTNKNQFGIYNDKLSEVNISQNDIYDNKYKNFSISFWVRIPNYDNKIVN--VNNE 939

 Query: 124 YTIINC MK-NNSWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDIS EYINRWFFVTIT 182
 YTIINC M+NNSWK+S+ N ITWTL D +G + + F Y TS+YIN+W FVTIT
 Sbjct: 940 YTIINC RDNNNSGWKVSLNHNEIIWTLQDNGINQKLAFNYGNANGISDYINKWIFVTIT 999

 Query: 183 NN-LNNAKIYI NGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQF IWMKYFSIFNTELS 241
 N+ L ++K+YING L I ++ + + I+FK+ + T++I ++YF+IF+ EL
 Sbjct: 1000 NDRLGDSKLYINGNLIDKKSILNLGNIHVDNILFKI-VNC SYTRYIGIRYFNIFDKELD 1058

 Query: 242 QSNIEERYKIQSSEYLKD FWGNPLM YNKEYY MFNAGN KNS YIKL KKDS PVGE ILTR SKY 301
 ++ I+ Y + + LKDFWGN L+Y+KEYY+ N N++I + DS T S
 Sbjct: 1059 ETEIQTLYNNEPNANILKDFWGNYLLYDKEYYLLNVLKPNNFINRRRTDS-----TLSIN 1112

 Query: 302 NQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRYTXXXXX 361
 N S + LY G K I+R +NS S ND++VRK D +Y++F + + +
 Sbjct: 1113 NIRSTILLANRLYSGIKVKIQRVNNS-STNDNLVRKNDQVYINF--VASKTHLLPLYADT 1169

 Query: 362 XXXXXXXXAPISDSDEFYNTIQIKEYDEQPTYS CQLLF KKDEESTDEIGLIGIHRFYESG 421
 IS S +N + + +C + FK + + + IGL+G
 Sbjct: 1170 ATTNKEKTIKISSSGNRFNQVVVM---NSVGNCTMNFKN--NGNNIGLLGFK----- 1218

 Query: 422 IVFEEYKDYFCISKWYLKEVKRKPYNLKG CNWQFIPKDEGWTE 465

N+ L ++K+YING L I ++ + + I+FK+ + T++I ++YF+IF+ EL
 Sbjct: 996 NDRLGDSKLYINGNLIDKKSILNLGNIHVSNDNILFKI-VNC SYTRYIGIRYFNIFDKELD 1054

Query: 242 QSNIEERYKIQSSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKY 301
 ++ I+ Y + + LKDFWGN L+Y+KEYY+ N N++I + DS T S
 Sbjct: 1055 ETEIQTLYNNEPNANILKDFWGNYLLYDKEYYLLNVLKPNNFINRRTDS-----TLSIN 1108

Query: 302 NQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYXXXXX 361
 N S + LY G K I+R +NS S ND++VRK D +Y++F + + +
 Sbjct: 1109 NIRSTILLANRLYSGIKVKIQRVNNS-STNDNLVRKNDQVYINF--VASKTHLLPLYADT 1165

Query: 362 XXXXXXXXAPISDSDEFYNTIQIKEYDEQPTYSQOLLFKKDEESTDEIGLIGIHRFYESG 421
 IS S +N + + +C + FK + + + IGL+G
 Sbjct: 1166 ATTNEKEKTIKISSSGNRFNQVVVM---NSVGNCTMNFKNN--NGNNIGLLGFK----- 1213

Query: 422 IVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE 465
 U S WY ++ + G W F I + + GW E
 Sbjct: 1214 -----ADTVVASTWYYTHMRDNTNS--NGFFWNFISEEHGWQE 1249

tr Q9FAR6 Type E botulinum toxin [bont/E] [Clostridium butyricum] 1255 AA
Q9FAR6_CLOBU
align

Score = 266 bits (679), Expect = 9e-70
 Identities = 161/464 (34%), Positives = 248/464 (52%), Gaps = 35/464 (7%)

Query: 6 LKTIMEFDLSIYTNDTILEMFNKYNSEXXXXXXXXXRYKDNNLIDLSSGYGAKVEVYDGV 65
 L +PF LS YT+D TLE FMK+ RYK++ +D SGY + + + V
 Sbjct: 822 LNNSIPFKLSSYTDDKILISYFNKFFKRIKSSSVLMRKYNDKYVDTSGYDSNININGDV 881

Query: 66 EL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFDFSVSFWIRIPKYKNDGIQNYIHNE 123
 +KNQF + + S++ ++QN TT+++ + +FS+SFW+RIF Y N + + +NE
 Sbjct: 882 YKYP TNKNQFGIYNDKLSEVNISQNDIYDNKYKNFSISFWVRIPNYDNKIVN--VNNE 939

Query: 124 YTIINC MK-NSG WKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTIT 182
 YTIINC M-NSG WK+S+ N IIWTL D +G + + Y Y IS+YIN+W FVTIT
 Sbjct: 940 YTIINC MRDNNSGWKVSLHN EIIWTLQDN SGINQKLA FNYGNANGISDYINKWIFVTIT 999

Query: 183 NN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNT ELS 241
 N+ L ++K+YING L I ++ + + I+FK+ + T++I ++YF+IF+ EL
 Sbjct: 1000 NDRLGDSKLYINGNLIDKKSILNLGNIHVSNDNILFKI-VNC SYTRYIGIRYFNIFDKELD 1058

Query: 242 QSNIEERYKIQSSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKY 301
 ++ I+ Y + + LKDFWGN L+Y+KEYY+ N N++I + DS T S
 Sbjct: 1059 ETEIQTLYNNEPNANILKDFWGNYLLYDKEYYLLNVLKPNNFINRRTDS-----TLSIN 1112

Query: 302 NQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYXXXXX 361
 N S + LY G K I+R +NS S ND++VRK D +Y++F + + +
 Sbjct: 1113 NIRSTILLANRLYSGIKVKIQRVNNS-STNDNLVRKNDQVYINF--VASKTHLLPLYADT 1169

Query: 362 XXXXXXXXAPISDSDEFYNTIQIKEYDEQPTYSQOLLFKKDEESTDEIGLIGIHRFYESG 421
 IS S +N + + +C + FK + + + IGL+G
 Sbjct: 1170 ATTNEKEKTIKISSSGNRFNQVVVM---NSVGNCTMNFKNN--NGNNIGLLGFK----- 1218

Query: 422 IVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE 465

D S W Y + + + G W F T + + G W E
 Sbjct: 1219 -----ADTVVASTWYYTHMRDNTNS--NGFFWNFISEEHGWQE 1254

tr Q8KZM3 Type E botulinum toxin [bont/E] [Clostridium butyricum] 1252 AA
 Q8KZM3_CLOBU
align

Score = 266 bits (679), Expect = 9e-70
 Identities = 161/464 (34%), Positives = 248/464 (52%), Gaps = 35/464 (7%)

Query: 6 LKTIMPFDSL IYTNDTILIE MFNKYNSE XXXXXXXX RYKDNNLIDL SGYGA KVEVYDG V 65
 L +PF LS YT+D ILI FNK+ RYK++ +D SGY + + + V
 Sbjct: 819 LNNSI PFKLSSYT DDKL ILYFNKFFKRIKSSSVLN MRYKNDK YVDTSGYDSNININGDV 878

Query: 66 EL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSF WIRIPKYKNDGIQNYIHNE 123
 +KNQF + + S++ + +QN IL++ + + +FS+SFW+RIP Y N + + +NE
 Sbjct: 879 YK YPTNKNQFGIYNDKLSEVNISQNDYIIYDNKYKNFSISFWVRIPNYDNKIVN--VNNE 936

Query: 124 YTII NC MK-NSG WKISIRGNRIIWTLIDINGKTKS VFFEY NIREDI SEY INRW FFV TIT 182
 YTII NC MK-NSG WK+S+ N IIWTL D +G + + F Y IS+YIN+W FV TIT
 Sbjct: 937 YTII INC MRDNN SGW KVSL NHNE IIWTLQDN SGINQKLAF NYGNANGISDYINKW IFV TIT 996

Query: 183 NN-LNNAKIYINGKLESNTDIK DIREVIANGEIIFKLDG D IDRTQF IWM KYFSI FNT ELS 241
 N+ L ++K+YING L I ++ + + T+FK+ + T++I ++YF+I F+ EL
 Sbjct: 997 NDRLG DSKLYINGNLIDKK SISL NLGNIH VSDN I LFKI-VNC SYTRYIGIRYF NI FDKE LD 1055

Query: 242 QSNIEERYKIQS YSEYLKD FWGNPLM YNKEY YM FNAGN KNS YIKL KK DS PVGE ILTR SKY 301
 ++ T+ Y + + LKDFWGN L+Y+KEYY+ N N++T + DS T S
 Sbjct: 1056 ETEIQ TLYNNEPNANILKDFWGN YLLDKEY YLLNVLKPNNFINRRTDS-----TLSIN 1109

Query: 302 NQNSKYINYRDLYIGEKFIIRRKSNSQ SINDDIVRKED YIYL DFFNLNQEW RVYXXXXX 361
 N S + LY G K T+R + NS S ND++VRK D +Y++F + + +
 Sbjct: 1110 NIRSTILLANRLYSGIKVKIQRVNNS-STNDNLVRKNDQVYINF--VASKTHLLPLYADT 1166

Query: 362 XXXXXXXXAPISDSDEFYNTIQIKEYDEQPTYSCQLLF KKDEESTDEI GLIGI HRF YESG 421
 IS S +N + + +C + FK + + + TGL+G
 Sbjct: 1167 ATTNKEKTIKISSSGNRFNQVVVM--NSVGNNCTMNFKNN--NGNNI GLLGFK----- 1215

Query: 422 IVFEE YKDYFCIS KWYLKEV KRKP YNLKG C NWQF IPK DEG WTE 465
 D S W Y + + + G W F T + + G W E
 Sbjct: 1216 -----ADTVVASTWYYTHMRDNTNS--NGFFWNFISEEHGWQE 1251

sp P19321 Botulinum neurotoxin type D precursor (EC 3.4.24.69) 1276
 BXD_CLOBO (BoNT/D) AA
 (Bontoxilysin D) [botD] [Clostridium botulinum]
align

Score = 233 bits (594), Expect = 7e-60
 Identities = 160/484 (33%), Positives = 244/484 (50%), Gaps = 61/484 (12%)

Query: 3 NKYLKTIMPFDLSIYTNDTILIE MFNKYNSE XXXXXXXX RYKDNNLIDL SGYGA KVEVY 62
 N+ + MPF++ YT N++FL ++ N+Y + + + K N L+D SGY A+V V
 Sbjct: 833 NESFENTMPFNIFS YTN SLLKDIINEYFNSINDSK ILSLQNK NALVDTSGYNAEV RVG 892

D S W Y + + + G W F T + + G W E
 Sbjct: 1219 -----ADTVVASTWYYTHMRDNTNS--NGFFWNFISEEHGWQE 1254

tr Q8KZM3 Type E botulinum toxin [bont/E] [Clostridium butyricum] 1252 AA
 Q8KZM3_CLOBU

align

Score = 266 bits (679), Expect = 9e-70
 Identities = 161/464 (34%), Positives = 248/464 (52%), Gaps = 35/464 (7%)

Query: 6 LKTIMPFDLSIYTNDTILIEFMNKYNSEXXXXXXXXXRYKDNNLIDLSSGYGAKVEVYDGV 65
 Sbjct: 819 LNNSIPFKLSSYTDDKILISYFNKFFKRIKSSSVLNMRKYNDKYVDTSGYDSNININGDV 878

Query: 66 EL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFDFSVSFWRIPKYKNDGIQNYIHNE 123
 Sbjct: 879 YKYP TNKNQFGIYNDKLSEVNISQNDYIYDNKYKNFSISFWVRIPNYDNKIVN--VNNE 936

Query: 124 YTIIINC MK-NNSG WKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFVTIT 182
 Sbjct: 937 YTIIINC RDNN SGW KVSL NHNE IIWTLQD NSG INQ KLA F NY GNANG IS DYINK W IF VTIT 996

Query: 183 NN-LNNAKIYINGKLESNTDIKDIREVIANGEIIIFKLDGDIDRTQFIWMKYFSIFNTELS 241
 Sbjct: 997 NDRLG DSKLYINGNLIDKK S I L NL G NI H V SD N I L F K I - V NC SY TRY I G I R Y F N I F D K E L D 1055

Query: 242 QSNIEERYKIQS YSEYL KDFWGNPLMYNKEYYM FNAGN KNS YIKL KK D SPV GEIL TR SKY 301
 Sbjct: 1056 ETEI QTLYNNEPNANILKDFWGN YLL D KEY Y LL NVL K PNN FIN RRT DS-----TLSIN 1109

Query: 302 NQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEW RVYXXXXX 361
 Sbjct: 1110 NIRSTILLANRLYSGIKVKIQRVNNS-STNDNLVRKNDQVYINF--VASKTHLLPLYADT 1166

Query: 362 XXXXXXXXAPISDSDEFYNTIQIKEYDEQPTYS C Q L F K K D E E S T D E I G L I G I H R F Y E S G 421
 Sbjct: 1167 ATTNKEKTIKISSSGNRFNQVV M--NSVGN NCTMNF K N N--NGNNI GLG FK----- 1215

Query: 422 IVFEEYKDYFCISWKYLKEVKRKPYNLKG CNWQFIPKDEGWTE 465
 Sbjct: 1216 -----ADTVVASTWYYTHMRDNTNS--NGFFWNFISEEHGWQE 1251

sp P19321 Botulinum neurotoxin type D precursor (EC 3.4.24.69) 1276
 BXD_CLOBO (BoNT/D) AA
 (Bontoxilysin D) [botD] [Clostridium botulinum] align

Score = 233 bits (594), Expect = 7e-60
 Identities = 160/484 (33%), Positives = 244/484 (50%), Gaps = 61/484 (12%)

Query: 3 NKYLKTIMPF DLSIYTNDTILIEFMNKYNSEXXXXXXXXXRYKDNNLIDLSSGYGAKVEVY 62

Sbjct: 833 N E S F E N T M P F N I F S Y T N N S L L K D I I N E Y F N S I N D S K I L S L Q N K K N A L V D T S G Y N A E V R V G 892

Query: 63 DGVELND--KNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVFWIRIPKYKNDGIQNYI 120
 D V+LN N FKL+SS + KI V N NI++++++ + SVSEFWI+I K +
 Sbjct: 893 DNVQLNTIYTNDFKLSSSGD-KIIVNLNNNILYSAIYENSSVSFWIKISKDLTNS----- 946

Query: 121 HNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVT 180
 HNEYTIIN ++ NSGWK+ IR I W L D+N K KS+ F+Y+ + Y N+WFFVT
 Sbjct: 947 HNEYTIINSIEQNSGWKLCIRNGNIEWILOQDVNRKYKSLIFDYSESLSHTGYTNKWFFVT 1006

Query: 181 ITNNLNN-AKIYINGKLESNTDIKDIREVIANGEIIIFKLDGDidRTQFIFWMKYFSIFNTE 239
 ITNN+ K+YING+L+ + I+D+ EV + T+F +D +ID Q +W++ F+IF+ E
 Sbjct: 1007 ITNNNIMGYMKLYINGELKQSQKIEDLDEVKLDKTIVFGIDENIDENQMLWIRDFNIFSKE 1066

Query: 240 LSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRS 299
 LS +I Y+ Q +KD+WGNPL ++ EYY+ N + YI +P +L
 Sbjct: 1067 LSNEDINIVYEGOILRNVIKDYWGNPLKFDEYYIINDNYIDRYI-----APESNVLVLV 1121

Query: 300 KYNQNSKYINYRDLYIGEKFIIRRKSNSQSIINDDIVRKEDYIYLDFFNLNQEWRVYXXX 359
 +Y SK LY G I+ S+ + + D I L +***+
 Sbjct: 1122 QYPDRSK-----LYTGNPITIKSVSDKNPYSR--ILNGDNIIHLHMLYNSRKYMI----- 1168

Query: 360 XXXXXXXXXXXXAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGHR--- 416
 I D+D Y T Q E + Y+ +L + + IG+ I
 Sbjct: 1169 -----IRDTDTIYAT-QGGECSQNCVYALKL--QSNLGNYGIGIFSIKNIVS 1212

Query: 417 -----FYESGIVFEE-YKDYFCISKWYLKEVKRKPYNLKL---GCNWQFIPKDE 461
 F E+ ++ + YK + K V Y RL W+FT +D
 Sbjct: 1213 KNKYCSQIFSSFRENTMLLADIYKPWRFSFKNAYTPAVTNYETKLLSTSSFWKFISRDP 1272

Query: 462 GWTE 465
 GW E
 Sbjct: 1273 GWVE 1276

tr Q9QTG7 NTX (Fragment) [ntx] [Clostridium botulinum D 1275
Q9QTG7_CBDP bacteriophage] AA
align

Score = 231 bits (590), Expect = 2e-59
 Identities = 132/338 (39%), Positives = 198/338 (58%), Gaps = 24/338 (7%)

Query: 3 NKYLKTIMPFDSLITYTNDTILLIEMFNKYNSEXXXXXXXXXRYKDNNNLIDLSGYGAKVEVY 62
 N+ + MPF++ YTN++L ++ N+Y + + K N L+D SGY A+V V
 Sbjct: 833 NESFENTMPFNIFSYTNNSSLKDIINEYFNSINDSKILSLQNNKALVDTSGYNAEVVRVG 892

Query: 63 DGVELND--KNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVFWIRIPKYKNDGIQNYI 120
 D V+LN N FKL+SS + KI V N NI++++++ + SVSEFWI+I K +
 Sbjct: 893 DNVQLNTIYTNDFKLSSSGD-KIIVNLNNNILYSAIYENSSVSFWIKISKDLTNS----- 946

Query: 121 HNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVT 180
 HNEYTIIN ++ NSGWK+ IR I W L D+N K KS+ F+Y+ + Y N+WFFVT
 Sbjct: 947 HNEYTIINSIEQNSGWKLCIRNGNIEWILOQDVNRKYKSLIFDYSESLSHTGYTNKWFFVT 1006

Query: 181 ITNNLNN-AKIYINGKLESNTDIKDIREVIANGEIIIFKLDGDidRTQFIFWMKYFSIFNTE 239
 ITNN+ K+YING+L+ + I+D+ EV + T+F +D +ID Q +W++ F+IF+ E
 Sbjct: 1007 ITNNNIMGYMKLYINGELKQSQKIEDLDEVKLDKTIVFGIDENIDENQMLWIRDFNIFSKE 1066

Query: 63 DGVELND--KNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYI 120
 D V+LN N EKI+SS + KI V N NI++++++ + SVSEWI+E K +
 Sbjct: 893 DNVQLNTIYTNDFKLSSSGD-KIIVNLNNNILYSAIYENSSVSFWIKISKDLTNS----- 946

Query: 121 HNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFV 180
 HNEYTIIN ++ NSGWK+ ER I W L D+N K KS+ F+Y+ + Y N+WFFV
 Sbjct: 947 HNEYTIINSIEQNSGWKLCIRNGNIEWILOQDVNRKYKSLIFDYSESLSHTGYTNKWFFV 1006

Query: 181 ITNNLNN-AKIYINGKLESNTDIKDIREVIANGEIIFKLDGDidRTQFIWMKYFSIFNTE 239
 ITNN+ K+YING+L+ + I+D+ EV + T+F +D +ID Q +W++ F+I+F+ E
 Sbjct: 1007 ITNNIMGYMKLYINGELKQSQKIEDLDEVKLDKTIVFGIDENIDENQMLWIRDFNIFSKE 1066

Query: 240 LSQSNIIEERYKIQSSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKDDSPVGEILTRS 299
 LS +I Y+ Q +KD+WGNPL ++ EYY+ N + YI +P +L
 Sbjct: 1067 LSNEDINIVYEGQILRNVIKDYWGNPLKFDEYYIINDNYIDRYI----APESNLVLV 1121

Query: 300 KYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYXXX 359
 +Y SK LY G I+ S+ + + D I L +++++ +
 Sbjct: 1122 QYPDRSK-----LYTGNPITIKSVDKNPYSR--ILNGDNIILHMLYNSRKYMI----- 1168

Query: 360 XXXXXXXXXAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGHR--- 416
 I D+D Y T Q E + Y+ +L + + IGP+ I
 Sbjct: 1169 -----IRDTDTIYAT-QGGECSQNCVYALKL---QSNLGNYGIGIFSIKNIVS 1212

Query: 417 -----FYESGIVFEE-YKDYFCISKWYLKEVKRKPYNLKL---GCNWQFIPKDE 461
 P E+ ++ + YK + K V Y EL W+F+ +D
 Sbjct: 1213 KNKYCSQIFSSFRENTMALLADIYKPWRFSFKNAYTPAVTNYETKLLSTSSFWKFISRDP 1272

Query: 462 GWTE 465
 GW E
 Sbjct: 1273 GWVE 1276

tr Q9QTG7 NTX (Fragment) [ntx] [clostridium botulinum D] 1275
Q9QTG7_CBDP bacteriophage AA
align

Score = 231 bits (590), Expect = 2e-59
 Identities = 132/338 (39%), Positives = 198/338 (58%), Gaps = 24/338 (7%)

Query: 3 NKYLKTIMPDFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXRYKDNNNLIDLSGYGAKVEVY 62
 N+ + MPF++ YTN+++L ++ N+Y + + K N L+D SGY A+V V
 Sbjct: 833 NESFENTMPFNIFSYTNNSSLKDIINEYFNSINDSKILSLQNNKNALVDTSGYNAEVVRG 892

Query: 63 DGVELND--KNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYI 120
 D V+LN N EKI+SS + KI V N NI++++++ + SVSEWI+E K +
 Sbjct: 893 DNVQLNTIYTNDFKLSSSGD-KIIVNLNNNILYSAIYENSSVSFWIKISKDLTNS----- 946

Query: 121 HNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFV 180
 HNEYTIIN ++ NSGWK+ ER I W L D+N K KS+ F+Y+ + Y N+WFFV
 Sbjct: 947 HNEYTIINSIEQNSGWKLCIRNGNIEWILOQDVNRKYKSLIFDYSESLSHTGYTNKWFFV 1006

Query: 181 ITNNLNN-AKIYINGKLESNTDIKDIREVIANGEIIFKLDGDidRTQFIWMKYFSIFNTE 239
 ITNN+ K+YING+L+ + I+D+ EV + T+F +D +ID Q +W++ F+I+F+ E
 Sbjct: 1007 ITNNIMGYMKLYINGELKQSQKIEDLDEVKLDKTIVFGIDENIDENQMLWIRDFNIFSKE 1066

Query: 240 LSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRS 299
 LS +I Y+ Q +KD+WGNPL ++ EYYM N + YI +P TL
 Sbjct: 1067 LSNEDINIVYEGQILRNVIKDYWGNPLKFDEYYIINDNYIDRYI----APESNVLV 1121

Query: 300 KYNQNSKYINYRDLYIGEKFIIRRKSNSQIN-DDIVRKEDYIYLDFFNLNQEWRVYTX 338
 +Y SK LY G I+ S+ S+ +N D
 Sbjct: 1122 QYPDRSK-----LYTGNPITIKSVSDKNPYSRILNGD 1153

tr Q5DW55 Type C botulinaum neurotoxin [bont/C] [Clostridium] 1280
Q5DW55_CLOBO botulinum AA
align

Score = 230 bits (586), Expect = 6e-59
 Identities = 153/469 (32%), Positives = 240/469 (50%), Gaps = 31/469 (6%)

Query: 3 NKYLKTIMPFDLSIYTNDTILIEFMFNKYNSEXXXXXXXXXRYKDNNLIDLSSGYGAKVEVY 62
 N+ + +PF++ YTN++L ++ N+Y + + K N L+D SGY A+V +
 Sbjct: 837 NESFENTIPFNIFSYTNNSSLKDIINEYFNSINDSKILSLQNNKALVDTSGYNAEVRL 896

Query: 63 DGVELND--KNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGQNYI 120
 V++N N FKL+SS + KI V N NI+++ + SVSFWI+L X +
 Sbjct: 897 GDVQVNNTIYTNDFKLSSSGD-KIIVNLNNNILYSAIYENSSVSFWIKISKDLTNS---- 950

Query: 121 HNEYTIINC MKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVT 180
 HNEYTIIN +K NSCWK+ IR I W L DTN K ES+ F+Y+ + Y N+WFVFVT
 Sbjct: 951 HNEYTIINSI昆QNSGWKLCIRNGNIEWILOQDINRKYKSLIFDYSESLSHTGYTNKWFFVT 1010

Query: 181 ITNNLNN-AKIYINGKLESNTDIKDIREVIANGEIIIFKLDGDIDRTQFQIWMKYFSIFNTE 239
 ITNN+ K+YING+L+ + I+D+ EV + T+F +D +TD Q +W++ F+IF+ E
 Sbjct: 1011 ITNNIMGYMKLYINGELKQSERIEDLDEVKLDKTIVFGIDENIDENQMLWIRDFNFSKE 1070

Query: 240 LSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRS 299
 LS +I Y+ Q +KD+WGNPL ++ EYYM N + YI +P TL
 Sbjct: 1071 LSNEDINIVYEGQILRNVIKDYWGNPLKFDEYYMINNYIDRYI----APKNNILV 1125

Query: 300 KYNQNSKYINYRDLYIGEKFIIRRKSNSQIN-DDIVRKEDYIYLDFFNLNQEWRVYTX 358
 +Y SK + I K + S+ +N DDI+ Y ++ + +Y
 Sbjct: 1126 QYSDISKLYTKNPITI--KSAANKNPYSRILNGDDIMFHMLYDSREYMIIRDTDTIYATQ 1183

Query: 359 XXXXXXXXXXXXAPISDSDEFY--NTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGHR 416
 + + Y TK Q Y C +F +T + L T++
 Sbjct: 1184 GGQCSKNCVYALKLQSNLGNYGIGIFSIKNIVSQNKY-CSQIFSSFMKNT--MLLADIYK 1240

Query: 417 FYESGIVFEEYKDYFCISWKYLKEVKRKPYNLKLGCNWQFIPKDEGWTE 465
 + F S + + + K + + W+YI +D GW S
 Sbjct: 1241 PWR--FSFENAYTPVAVTNYETKLLSTSSF-----WKFISRDPGWVE 1280

tr Q9LBS7 Type C botulinaum neurotoxin [bont/C] [Clostridium] 1280
Q9LBS7_CLOBO botulinum AA
align

Score = 228 bits (580), Expect = 3e-58
 Identities = 131/338 (38%), Positives = 197/338 (57%), Gaps = 24/338 (7%)

Query: 240 LSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKN SYIKLKKDSPVGEILTRS 299
 LS +I Y+ Q +KD+WGNPL ++ EYYM N + XI +P +L
 Sbjct: 1067 LSNEDINIVYEGQILRNVIKDYWGNPLKFDEYYIINDNYIDRYI----APESNLVLV 1121

Query: 300 KYNQNSKYINYRDLYIGEKFIIRRKSNSQSIN-DDIVRKEDYIYLDFFNLNQEWRVYTX 333
 +Y SK IY G I+ S+ S+ +W D
 Sbjct: 1122 QYPDRSK-----LYTGNPITIKSVSDKNPYSRILNGD 1153

tr Q5DW55 Type C botulinum neurotoxin [bont/C] [Clostridium] 1280
Q5DW55_CLOBO botulinum AA
align

Score = 230 bits (586), Expect = 6e-59
 Identities = 153/469 (32%), Positives = 240/469 (50%), Gaps = 31/469 (6%)

Query: 3 NKYLKTIMPFDLSIYTNDTILIEFMNKYNSEXXXXXXXXXRYKDNNNLIDL SGY GAKVEVY 62
 N+ + +PF++ YTN++L ++ N+Y + + K N L+D SGY A+V +
 Sbjct: 837 NESFENTIPFNIFSYTNNSSLKDIINEYFNSINDSKILSLQNKNALVDTSGYNAEVRL 896

Query: 63 DGVELND--KNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGQNYI 120
 V++N N FKL+SS + KI V N NI++++++ + SVSEWI+I K +
 Sbjct: 897 GDVQVN TITYTNDFKLSSSGD-KIIVNLNNNILYSAIYENSSVSFWIKISKDLTNS---- 950

Query: 121 HNEYTIINC MKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVT 180
 HNEYTIIN +K NSCWK+ IR I W L DIN K KS+ F+Y+ + Y N+WF FVT
 Sbjct: 951 HNEYTIINSIKQNSG WKLCIRNGNIEWILOQDINRKYKSLIFDYSESLSHTGYTNKWF FVT 1010

Query: 181 ITNNLNN-AKIYINGKLESNTDIKDIREVIANGEIIIFKLDGDIDRTQFIWMKYFSIFNTE 239
 ITNN+ K+YING+L+ + I+D+ EV + I+F+D +ID Q +W++ F+IF+ E
 Sbjct: 1011 ITNNIMGYMKLYINGELKQSERIEDLDEVKLDKTIVFGIDENIDENQMLWIRDFNIFSKE 1070

Query: 240 LSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKN SYIKLKKDSPVGEILTRS 299
 LS +I Y+ Q +KD+WGNPL ++ EYYM N + XI +P +L
 Sbjct: 1071 LSNEDINIVYEGQILRNVIKDYWGNPLKFDEYYMINYIDRYI----APKNNILVLV 1125

Query: 300 KYNQNSKYINYRDLYIGEKFIIRRKSNSQSIN-DDIVRKEDYIYLDFFNLNQEWRVYTX 358
 +Y+ SK + I K + S+ +N DDE+ Y + + + +Y
 Sbjct: 1126 QYSDISKLYTKNPITI--KSAANKNPYSRILNGDDIMFHMLYDSREYMIIRD TDTIYATQ 1183

Query: 359 XXXXXXXXXXXXAPISDSDEFY--NTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHR 416
 + + Y TK Q Y C +F + +T + L I++
 Sbjct: 1184 GGQCSKNCVYALKLQSNLGNYGIGIFS IKNIVSQNKY-CSQIFSSFMKNT--MLLADIYK 1240

Query: 417 FYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLCNCNWQFIPKDEGWTE 465
 + F E + + + K + + W+F+D GW E
 Sbjct: 1241 PWR--FSFENAYTPVAVTNYETKLLSTSSF-----WKFISRDPGWVE 1280

tr Q9LBS7 Type C botulinum neurotoxin [bont/C] [Clostridium] 1280
Q9LBS7_CLOBO botulinum AA
align

Score = 228 bits (580), Expect = 3e-58
 Identities = 131/338 (38%), Positives = 197/338 (57%), Gaps = 24/338 (7%)

Query: 3 NKYLKTIMPFDSLISYTNDTILIEFMNKYNSEXXXXXXXXXRYKDNNLIDLSGYAKVEVY 62
Sbjct: 837 NESFENTIPFNIFSYTNNSLKDIINEYFNSINDSKILSLQNKKNALVDTSGYNAEVRL 896

Query: 63 DGVELND--KNQFKLTSSANSKIRVTQNQNIIFNSVFLLDFSVFWIRIPKYKNDGIQNYI 120
Sbjct: 897 GDVQVNТИYTNDFKLSSSGD-KIIVNLNNNLYSAIYENSSVSFWIKISKDLTNS---- 950

Query: 121 HNEYTIINCMKNNSGKISIRGNRIIWTLIDINGKTGSVFFEYNIREDISEYINRWFFVT 180
Sbjct: 951 HNEYTIINSIKQNSGKLCIRNGNIEWIЛQDINRKYKSLIFDYSELSHTGYTNKWFV 1010

Query: 181 ITNNLNN-AKIYINGKLESNTDIKDIREVIANGEIIIFKLDGDIDRTQFIWMKYFSIFNTE 239
Sbjct: 1011 ITNNIMGYMKLYINGELKQSERIEDLNEVKLDKTIVFGIDENIDENQMLWIRDFNIFSKE 1070

Query: 240 LSQSNIIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRS 299
Sbjct: 1071 LSNEDINIVYEGQILRNVIKDYWGNPLKFDEYYIINDNYIDRYI----APKSNILVLV 1125

Query: 300 KYNQNSKYINYRDLYIGEKFIIRRKSN---SQSINDD 333
Sbjct: 1126 QYPDRSK----LYTGNPITIKSVSDKNPYSRILNGD 1157

tr Q45849 Neurotoxin [Clostridium botulinum C] 1280 AA
 Q45849_CLOBO align
 Score = 228 bits (580), Expect = 3e-58
 Identities = 131/338 (38%), Positives = 197/338 (57%), Gaps = 24/338 (7%)
 Query: 3 NKYLKTIMPFDLSIYTNDTILIEFMNKYNSEXXXXXXXXXRYKDNNLIDLSGYAKVEVY 62
 Sbjct: 837 N+ + +PF++ YTM+++L ++ N+Y + + K N L+D SGY A+V + NESFENTIPFNIFSNTNNSSLKDIINEYFNSINDSKILSLQNKNALVDTSGYNAEVRL 896
 Query: 63 DGVELND--KNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWRIPKYKNDGIQNYI 120
 Sbjct: 897 V++N N FKL+SS + KI V N NI++++++ + SVSFWI+I K + GDVQVNТИYTNDFKLSSSGD-KIIVNLNNNILYSAIYENSSVSFWIKISKDLTNS---- 950
 Query: 121 HNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFV 180
 Sbjct: 951 HNEYTIINNSIKQNSGWKLCIRNGNIEWILQDINRKYKSLIFDYSESLSHTGYTNKWFV 1010
 Query: 181 ITNNLNN-AKIYINGKLESNTDIKDIREVIANGEIIFKLDGDDIDRTQFIWMKYFSIFNTE 239
 Sbjct: 1011 ITNNIMGYMKLYINGELKQSERIEDLNEVKLDKTIVFGIDENIDENQMLWIRDFNIFSKE 1070
 Query: 240 LSQSNIIEERYKIQSYSEYLKDFWGNPLMYNKEYMFNAGNKNSYIKLKKDSPVGEILTRS 299
 Sbjct: 1071 LSNEDINIVYEGQILRNVIKDYWGPNPLKFDEYYIINDNYIDRYI----APKSNILVLV 1125
 Query: 300 KYNQNSKYINYRDLYIGEKFIIRRKSN---SQSINDD 333
 Sbjct: 1126 +Y SK LY G I+ S+ S+ +N D QYPDRSK-----LYTGNPITIKSVSDKNPYSRILNGD 1157

Query: 3 NKYLKTIMPFDSLISYTNDTILIEMFNKYNSEXXXXXXXXXRYKDNNLIDLSGYGAKVEVY 62
 N+ + +PF++ YTN+++: ++ N+Y + + K N L+D SGY A+V +
 Sbjct: 837 NESFENTIPFNIFSYTNNSSLKDIINEYFNSINDSKILSLQNKNALVDTSGYNAEVRL 896

Query: 63 DGVELND--KNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFIRIPKYKNDGIQNYI 120
 V++N N FKL+SS + KT V N NI++++++ + SVSFWI+i K +
 Sbjct: 897 GDVQVNNTIYTNDFKLSSSGD-KIIVNLNNNLYSAIYENSSVSFWIKISKDLTN----- 950

Query: 121 HNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFV 180
 HNEYTIIN +K NSGWK+ TR I W L DIN K KS+ F+Y+ + X N+WFFV
 Sbjct: 951 HNEYTIINSIKQNSGWKLCIRNGNIEWILQDINRKYKSLIFDYSESLSHTGYTNKWFFV 1010

Query: 181 ITNNLNN-AKIYINGKLESNTDIKDIREVIANGEIIIFKLDGDIDRTQFQIWMKYFSIFNTE 239
 ITNN+ K+YING+L+ + I+D+ EV + I+F +D +ID Q +W++ F+T+ E
 Sbjct: 1011 ITNNIMGYMKLYINGELKQSERIEDLNEVKLDKTIVFGIDENIDENQMLWIRDFNIFSKE 1070

Query: 240 LSQSNIIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRS 299
 LS +I Y+ Q +KD+WGPNPL ++ EYY+ N + YT +P IL
 Sbjct: 1071 LSNEDINIVYEGQILRNVIKDYWGNPLKFDEYYIINDNYIDRYI-----APKSNILVLV 1125

Query: 300 KYNQNSKYINYRDLYIGEKFIIRRKSN---SQSINDD 333
 +Y SK LY G I+ S+ S+ +N D
 Sbjct: 1126 QYPDRSK-----LYTGNPITIKSVSDKNPYSRILNGD 1157

tr Q45849 **Neurotoxin [Clostridium botulinum C]** 1280 AA
Q45849_CLOBO align

Score = 228 bits (580), Expect = 3e-58
 Identities = 131/338 (38%), Positives = 197/338 (57%), Gaps = 24/338 (7%)

Query: 3 NKYLKTIMPFDSLISYTNDTILIEMFNKYNSEXXXXXXXXXRYKDNNLIDLSGYGAKVEVY 62
 N+ + +PF++ YTN+++: ++ N+Y + + K N L+D SGY A+V +
 Sbjct: 837 NESFENTIPFNIFSYTNNSSLKDIINEYFNSINDSKILSLQNKNALVDTSGYNAEVRL 896

Query: 63 DGVELND--KNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFIRIPKYKNDGIQNYI 120
 V++N N FKL+SS + KT V N NI++++++ + SVSFWI+i K +
 Sbjct: 897 GDVQVNNTIYTNDFKLSSSGD-KIIVNLNNNLYSAIYENSSVSFWIKISKDLTN----- 950

Query: 121 HNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFV 180
 HNEYTIIN +K NSGWK+ TR I W L DIN K KS+ F+Y+ + X N+WFFV
 Sbjct: 951 HNEYTIINSIKQNSGWKLCIRNGNIEWILQDINRKYKSLIFDYSESLSHTGYTNKWFFV 1010

Query: 181 ITNNLNN-AKIYINGKLESNTDIKDIREVIANGEIIIFKLDGDIDRTQFQIWMKYFSIFNTE 239
 ITNN+ K+YING+L+ + I+D+ EV + I+F +D +ID Q +W++ F+T+ E
 Sbjct: 1011 ITNNIMGYMKLYINGELKQSERIEDLNEVKLDKTIVFGIDENIDENQMLWIRDFNIFSKE 1070

Query: 240 LSQSNIIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRS 299
 LS +I Y+ Q +KD+WGPNPL ++ EYY+ N + YT +P IL
 Sbjct: 1071 LSNEDINIVYEGQILRNVIKDYWGNPLKFDEYYIINDNYIDRYI-----APKSNILVLV 1125

Query: 300 KYNQNSKYINYRDLYIGEKFIIRRKSN---SQSINDD 333
 +Y SK LY G I+ S+ S+ +N D
 Sbjct: 1126 QYPDRSK-----LYTGNPITIKSVSDKNPYSRILNGD 1157

tr Q841S3 Neurotoxin [Clostridium botulinum] 1280 AA
 Q841S3_CLOBO align

Score = 226 bits (577), Expect = 6e-58
 Identities = 131/338 (38%), Positives = 196/338 (57%), Gaps = 24/338 (7%)

Query: 3 NKYLKTIMPFDLSIYTNDTILIEMFNKNYNSXXXXXXXXXRYKDNNLIDLSSGYGAKVEVY 62
 Sbjct: 837 NGSFENTIPFNIFSYTNNSLLKDIINEYFNSINDSKILSLQNKKNALVDTSGYNAEVRL 896

Query: 63 DGVELND--KNQFKLTSSANSKIRVTQNQNIIFNSVFLLDFSVSFWIRIPKYKNDGIQNYI 120
 Sbjct: 897 V++N N FKL+SS + KT V N NI++++++ + SVSFWI+I K +
 GDVQVNTIYTNDFKLSSSGD-KIIVNLNNNILYSAIYENSSVSFWIKISKDLTNS----- 950

Query: 121 HNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVT 180
 Sbjct: 951 HNEYTIIN +K NSGWK+ TR I W L DIN K KS+ P+Y+ + Y N+WFFVT
 HNEYTIINSIKQNSGWKLCIRNGNIEWILQDINRKYKSLIFDYSESLSHTGYTNKWFFVT 1010

Query: 181 ITNNLNN-AKIYINGKLESNTDIKDIREVIANGEIIFKLDGDDIDRTQFIWMKYFSIFNTE 239
 Sbjct: 1011 ITNNIMGYMKLYINGELKQSERIEDLNEVKLDKTIVFGIDENIDENQMLWIRDFNIFSKE 1070

Query: 240 LSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNYSIKLKKDSPVGEILTRS 299
 Sbjct: 1071 LSNDINIVYEGQILRNVIKDYWGNPLKFDTTEYYIINDNYIDRYI-----APKSNILVLV 1125

Query: 300 KYNQNSKYINYRDLYIGEKFIIRRKSNS---SQSINDD 333
 Sbjct: 1126 +Y SK LY G I+ S+ S+ +N D
 QYPDRSK-----LYTGNPITIKSVSDKNPYSRILNGD 1157

sp P04958 Tetanus toxin precursor (EC 3.4.24.68) (Tentoxylisin) 1314
TETX_CLOTE [Contains:
 Tetanus toxin light chain (Tetanus toxin chain L); AA
 Tetanus toxin heavy chain (Tetanus toxin chain H)] [tetX] align
 [Clostridium tetani]

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Score = 211 bits (538), Expect = 2e-53
Identities = 137/434 (31%), Positives = 222/434 (50%), Gaps = 27/434 (6%)

Query: 46 DNNLI-DLSGYGAKVEVYDGVEL----NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDF 100
       +N++I D+SG+ + V Y +L N K L ++ +S++ V + +T +N +F +F
Sbjct: 891 NNDIISDISGFNSSVITYPDAQLVPGINGK-AIHVLVNNESSEVIVHKAMDIEYNDMFNNF 949

Query: 101 SVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNS----GWKISIRGNRIIWTLIDINGK 155
       +VSFW+R+PK ++ Y NEY+II+ MK +S GW +S++GN +IWTL D G+
Sbjct: 950 TVSFWLRVPKVSAHLEQYGTNEYSIISSMKKHSLSIGSGWSVSLKGNNLIWTLKDSAGE 1009

Query: 156 TKSVF FEYNIREDISEYI-NRWFFVTITNN-LNNAKIYINGKLESNTDIKDIREVIANGE 213
       + + F + + + + Y+ N+W F+TITN+ L+A +YING L + +I + + +
Sbjct: 1010 VRQITFR-DLPDKFNAYLANKWVFITITNDRLSSANLYINGVLMGSAEITGLGAIREDNN 1068

Query: 214 IIFKLDGDDIDRTQFIFWMKYFSIFNTELSQNSNIEERYKIQSYSYSEYLKDFWGPNPLMYNKEYY 273
       I KLD + Q++ + F IF L+ +IE+ Y +L+DFWGPNPL Y+ EYY
Sbjct: 1069 ITLKLDRCNNNNQYVSIDKFRIFCKALNPKEIEKLYTSYLSITFLRDFWGPNPLRYDTEYY 1128

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tr Q841S3 Neurotoxin [Clostridium botulinum] 1280 AA
 Q841S3_CLOBO align

Score = 226 bits (577), Expect = 6e-58
 Identities = 131/338 (38%), Positives = 196/338 (57%), Gaps = 24/338 (7%)

Query: 3 NKYLKTIMPFDLSIYTNDTILIEMFNKNYNEXXXXXXXXXRYKDNNNLIDLSGYGAKEVY 62
 Sbjct: 837 NGSFENTIPFNIFSYTNNSSLKDIIINEYFNSINDSKILSLQNKKNALVDTSGYNAEVRL 896

Query: 63 DGVELND--KNQFKLTSSANSKIRVTQNQNIIFNSVFLLDFSVSFWIRIPKYKNDGIQNYI 120
 Sbjct: 897 DVQVNNTIYTNDFKLSSGD-KIIVNLNNNLYSAIYENSSVSFWIKISKDLTNS---- 950

Query: 121 HNEYTIINCMKNNSGWKISIRGNRIIWTLLIDINGKTKSVFFEYNIREDISEYINRWFFVT 180
 Sbjct: 951 HNEYTIINSIKQNSGWKLICIRNGNIEWILQDINRKYKSLIFDYSESLSHTGYTNKWFFVT 1010

Query: 181 ITNNLNN-AKIYINGKLESNTDIKDIREVIANGEIIFKLDGDDIDRTQFIWMKYFSIFNTE 239
 Sbjct: 1011 ITNNIMGYMKLYINGELKQSERIEDLNEVKLDKTIVFGIDENIDENQMLWIRDFNIFSKE 1070

Query: 240 LSQSNIEERYKIQSYSEYLKDWFGNPLMYNKEYMFNAGNKNYSIKLKKDSPVGEILTRS 299
 Sbjct: 1071 LSNEDINIVYEGQILRNVIKDYWGNPLKFDTVEYYIINDNYIDRYI----APKSNILVLV 1125

Query: 300 KYNQNSKYINYRDLYIGEKFIIRRKSNS---SQSINDD 333
 Sbjct: 1126 QYPDRSK-----LYTGNPITIKSVSDKNPYSRILNGD 1157

sp P04958 Tetanus toxin precursor (EC 3.4.24.68) (Tentoxylysin) 1314
TETX_CLOTE [Contains:
Tetanus toxin light chain (Tetanus toxin chain L); align
Tetanus toxin heavy chain (Tetanus toxin chain H)] [tetx]
[Clostridium tetani]

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Score = 211 bits (538), Expect = 2e-53
Identities = 137/434 (31%), Positives = 222/434 (50%), Gaps = 27/434 (6%)

Query: 46 DNNLI-DLSGYGAKVEVYDGVEL----NDKNQFKLTSSANSKIRVTQNQNIIIFNSVFLDF 100
       +N++T D+SG+ + V Y +L N K L ++ +S++ V + +I +N +F +E
Sbjct: 891 NNDIISDISGFNSSVITYPDAQLVPGINGK-AIHLVNNESSEVIVHKAMDIEYNDMFNNF 949

Query: 101 SVSFWIRIPKYKNDGIQNYIHNEYTIINC MKNNS----GWKISIRGNRIIWTLIDINGK 155
       +VSFW+R+PK ++ Y NEY+II+ MK +S GW +S++GN +IWTL D G+
Sbjct: 950 TVSFWLRLPKVSASHLEQYGTNEYSIISSM KKHSLSIGSGWSVSLKGNNLIWTLKDSAGE 1009

Query: 156 TKSVFFEYNIREDISEYI-NRWFFVTITNN-LNNAKIYINGKLESNTDIKDIREVIANGE 213
       + + F ++ + + Y+ N+W F+TITNN+ L++A +YING I + +I + + +
Sbjct: 1010 VRQITFR-DLPDKFNAYLANKWVFITITNDRLSSANLYINGVLMGSAEITGLGAIREDNN 1068

Query: 214 IIFKLDG DIDRTQFIWMKYFSIFNTELSQS NIEERYKIQSYSEYLKDFWGNPLMYNKEYY 273
       I KLD + Q++ + F IF L+ IEE+ Y +L+DFWGNPL Y+ EYY
Sbjct: 1069 ITLKLDRCNNNOYVSIDKFRI FCKALNPKEIEKLYTSYLSITEFLRDFWGNPLRYDTEYY 1128

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Query: 274 MFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIIRRKSNSQSINDD 333
+ + + ++LK + + Y I XR LY G KEIII+R + + I D
Sbjct: 1129 LIPVASSSKDVQLKNITDYMILTNAPSYTNGKLNIIYYRRLYNGLKFIIKRYTPNNEI-DS 1187

Query: 334 IVRKEDYIYLDFFNLNQEWRVYXXXXXXXXXXAPI---SDSDEFYNTIQIKEYDEQ 390
V+ D+I L N E V + + X ++ + +
Sbjct: 1188 FVKSGDFIKLYVSYNNEHIVGYPKDGNAFNNLDRILRVGYNAPGIPLYKKMEAVKLRDL 1247

Query: 391 PTYSCQLLFKKDEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKL 450
TYS QL D+ ++ +GL+G R I + +D S WY +K K L
Sbjct: 1248 KTYSVQLKLYDDKNAS--LGLVGTH---NGQIGNDPNRDILIASNWYFNHLKDK---IL 1298

Query: 451 GCNWQFIPKDEGWT 464
GC+W F+P DEGWT
Sbjct: 1299 GCDWYFVPTDEGWT 1312

tr Q9LA13 Tetanus toxin (Fragment) [Clostridium
 Q9LA13_CLOTE tetani] 451 AA
 align
 Score = 211 bits (536), Expect = 4e-53
 Identities = 137/434 (31%), Positives = 220/434 (50%), Gaps = 27/434 (6%)
 Query: 46 DNNLI-DLSGYGAKVEVYDGVEL----NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDF 100
 +N++I D+SG+ + V X +L N K L: ++ +S++ V + +I +N +S +P
 Sbjct: 28 NNDIISDISGFNNSVITYPDAQLVPGINGK-AIHLVNNESSEVIVHAKMDIEYNDMFNNF 86
 Query: 101 SVSFWIRIPKYKNDGIQNYIHNEYTIINCMKN----NSGWKISIRGNRIIWTLIDINGK 155
 +VSEW+R+PK ++ Y NEY+II+ MK SGW +S++GN +IWPL D G+
 Sbjct: 87 TVSFWLRVPKVASHLEQYDTNEYSIISSMKKYSLSIGSGWSVSLKGNNLIWTLKDSAGE 146
 Query: 156 TKSVFFEYNIREDISEYI-NRWFFVTITNN-LNNAKIYINGKLESNTDIKDIREVIANGE 213
 + + F ++ + + Y+ N+W F+TITN+ L+A +YING L + +I + + +
 Sbjct: 147 VRQITFR-DLSDKFNAYLANKWVFITITNDRLSSANLYINGVLMGSAEITGLGAIREDNN 205
 Query: 214 IIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGPNPLMYNKEYY 273
 I KID + Q++ + F IF L+ IE+ Y +L+DEWGNPL Y+ EYY
 Sbjct: 206 ITLKLDRCNNNNQYVSIDKFIFCKALNPKEIEKLYTSYLSITFLRDFWGPNPLRYDTEYY 265
 Query: 274 MFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDD 333
 + + ++LK + + Y I XR LY G KFII+R + + I D
 Sbjct: 266 LIPVAYSSKDVQLKNITDYMILTNAPSYTNGKLNIYYRRLYSGLKFIIKRYTPNNEI-DS 324
 Query: 334 IVRKEDYIYI LDFFNLNQEWRVYXXXXXXXXXXXXXAPI--SDSDEFYNTIQIKEYDEQ 390
 VR D+I L N E V . + + Y + ++ + +
 Sbjct: 325 FVRSGDFIKLYVSYNNEHIVGYPKDGNAFNNLDRILRGYNAPIPLYKKMEEAVKLRDL 384
 Query: 391 PTYSCQLLFKKDEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKL 450
 TYS QL D++++ +GL+G R I + +D S WY +K K L
 Sbjct: 385 KTYSVQLKLYDDKDAS--LGLVGTH--NGQIGNDPNRDILIASNWYFNHLKDK---TL 435
 Query: 451 GCNWQFIPKDEGWT 464
 C+W F+P DEGWT
 Sbjct: 436 TCDWYFVPTDEGWT 449

Query: 274 MFNAGNKNSYIKLKKDSPVGEILTRSKYQNQNSKYINYRDLYIGEKFIIIRKSNSQSINDD 333
+ + + ++LK + + Y I YR LY G KELI+R + + E D
Sbjct: 1129 LIPVASSSKDVQLKNITDYMILTNAPSYTNGKLNIIYRRLYNGLKFIIKRYTPNNEI-DS 1187

Query: 334 IVRKEDYIYLDFFNLNQEWRVYXXXXXXXXXXAPI---SDSDEFYNTIQIKEYDEQ 390
V+ D+T L N E V + + Y ++ + +
Sbjct: 1188 FVKSGDFIKLYVSYNNEHIVGYPKDGNAFNNLDRILRVGYNAPGIPLYKKMEAVKLRDL 1247

Query: 391 PTYS CQLLFKKDEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKL 450
TYS QL D+ ++ +GL+G H I + +D S WY +K K L
Sbjct: 1248 KTYSVQLKLYDDKNAS--LGLVGTH---NGQIGNDPNRDILIASNWYFNHLKDK---IL 1298

Query: 451 GCNWQFIPKDEGWT 464
GC+W F+P DEGWT
Sbjct: 1299 GCDWYFVPTDEGWT 1312

tr Q9LA13 Tetanus toxin (Fragment) [Clostridium 451 AA
Q9LA13 CLOTE tetani] align

Score = 211 bits (536), Expect = 4e-53
Identities = 137/434 (31%), Positives = 220/434 (50%), Gaps = 27/434 (6%)

Query: 46 DNNLI-DLSGYGAKEVYDGVEL---NDKNQFKLTSSANSKIRVTQNQNIIFNSVFDF 100
+N++E D+SG+ + V Y +L N E L ++ +S++ V + +I +N +F +P
Sbjct: 28 NNDIISDISGFNNSVITYPDAOLVPGINGK-AIHLVNNESEVIWHKAMDIEYNDMFNNF 86

Query: 101 SVSFWRIPKYKNDGIQNYIHNNEYTIINCMKN----NSGWKISIRGNRIIWTLIDINGK 155
+VSEW+R+PK + + Y NEY+LI+ MK SCW +S++GN +IWFL D G+
Sbjct: 87 TVSFWLRLPKVSASHLEQYDTNEYSIISSMKKYLSLIGSGWSVSILKGNNLIWTLKDSAGE 146

Query: 156 TKSVFNEYNIREDISEYI-NRWFFVTITNN-LNNAKIYINGKLESNTDIKDIREVIANGE 213
+ + + Y + + + Y + N+W S+TITN+ L+A +YING L + + I + + +
Sbjct: 147 VROITFR-DLSDKFNFAYLANKWVFITITNDRLSSANLYINGVLMGSAEITGLGAIREDNN 205

Query: 214 IIFKLDGDIDRTQFIWMKYFSIFNTELSQSNSIEERYKIQSYSEYLKDFTWGNPLMYNKEYY 273
I KLD + Q++ + F IF L+ IE+ Y +L+DFWGNEYL+ EYY
Sbjct: 206 ITILKLDRCNNNNNOVSIDKERIFCKALNPKEIEKLYTSLYSITFLRDFWGNEPLRYDTEYY 265

Query: 274 MFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKNSNSQSINDD 333
+ + + + EK + + Y T YR LY G KFII+R + + I D
Sbjct: 266 LTPVAYSSKDVLKNITDYMILTNAPSYTNGKLNIYYRRLLYSGLKFTIJKRYPTPNNET-DS 324

Query: 334 IVRKEDYIYLDFNLNQEWRVYXXXXXXXXXXXXAPI---SDSDEFYNTIQIKEYDEQ 390
 VR D+T L M E V + + Y ++ + +
 Sbj: 335 IVRKEDYIYLDFNLNQEWRVYXXXXXXXXXXXXAPI---SDSDEFYNTIQIKEYDEQ 390

Query: 391 PTYSQQLFKKDEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKL 450
TYS QL D++++ +GL+G R I + +D S WY +K K L

Query: 451 GCNWQFIPKDEGWT 464
C+W F+F DEGWT

Query: 451 GCNWQFIPKDEGWT 464
 C+W F+P DEGWT
Sbjct: 436 TCDWYFVPTDEGWT 449

tr Q45967 Neurotoxin consisting of botulinum neurotoxin D and C1 1285
 Q45967_CLOBO [Clostridium botulinum D] AA align

Score = 206 bits (523), Expect = 1e-51
 Identities = 150/480 (31%), Positives = 239/480 (49%), Gaps = 48/480 (10%)

Query: 3 NKYLKTIMPFDSL IYTNDTILIE FMNKYNSE XXXXXXXXRYKDNNLIDL SGYGA KVEVY 62
 N+ + +PF++ YTN++ +L +M N+Y + + + K N L+D SGY A+V V
 Sbjct: 833 NESFENTIPFNIFS YTNNSLLKDMINEYFNSINDSKILSLQNKKNTLM DTSGYNAEV RVE 892

Query: 63 DGVELND--KNQFKLTSSANS--KIRVTQNQNIIFNSVFLDFSVSF WIRIPKYKNDGIQN 118
 V+LN FKL SS + K+ VTQN+NI++N++ FS+SF WIRI K+ ++
 Sbjct: 893 GNVQLNP IFPFDFKLGSSGDDRGKIVITQNENIVNAMY EFSISFWIRINKWVSN--- 948

Query: 119 YIHNEYTIINCMKNNSGWKISIRGNRIWTLIDINGKTKSVFFEYNIREDISEYINRWFF 178
 YTII+ +KNNSGW I I N + + + T L + + + F Y+I ++ + Y N+WF F
 Sbjct: 949 --LPGYTIIDS VKNNSGWSIGIISNFLVFTLKQNENSEQDINF SYDISKNAAGY-NKWF F 1005

Query: 179 VTITNN-LNNAKIYINGKLESNTDIK DIREVIANGEIIFKLD-----GDIDRTQFI 228
 VTIT N + N IYINGKL +K++ + + I F++ + D D +
 Sbjct: 1006 VTITTNNMMGNMMIYINGKLIDTIKVKE LTGINFSKTITFQMNKIPNTGLITSDSDNIN-M 1064

Query: 229 WMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGPNPLMYNKEYYM FNAGN KNSYIKLKK 288
 W++ F IF EL +I + Y+ +KD+WGN L Y+KEYYM N N Y+ K
 Sbjct: 1065 WIRDFYIFAKELDDKDINILFNSLQYT NVVKDYWGNDLRYDKEYYMINVN YMNR YMSKG 1124

Query: 289 DSPVGEILTRSKYQNQSKYINYRDLYIGEKFII RKSNSQS INDDIVRKEDYIY LDFFNL 348
 + I+ + + N N D G K L+ + + ND VR E+ +Y +
 Sbjct: 1125 NG----IVFNTRKNNN-----DFNEG YKIIIKRIRG--NTNDTRVRGENVLYFNTTID 1171

Query: 349 NQEWR--VYTXXXXXXXXXXXAPISDSDEF--YNTIQIKEYDEQPTYS CQLL FKDEE 404
 N+++ +Y A DE Y+ I+ + Y+ Q LF
 Sbjct: 1172 NKQYSLGMYKPSRNLGTDLVPLGALDQPMDEIRKYGSFIIQPCNTFDYYASQ-LFLSSNA 1230

Query: 405 STDEIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKL---GCNWQFIPKDE 461
 +T+ +G++ I + F+ DY+ + + +K + Y L +W F+P E
 Sbjct: 1231 TTNR LGILSIGSY----SFKLGDDYWFNHEYLIPVIKIEHYASLLESTSTHWVFVPASE 1285

tr Q9LBRI Neurotoxin [Clostridium botulinum] 1285 AA
Q9LBRI_CLOBO align

Score = 205 bits (522), Expect = 1e-51
 Identities = 149/480 (31%), Positives = 239/480 (49%), Gaps = 48/480 (10%)

Query: 3 NKYLKTIMPFDSL IYTNDTILIE FMNKYNSE XXXXXXXXRYKDNNLIDL SGYGA KVEVY 62
 N+ + +PF++ YTN++ +L +M N+Y + + + K N L+D SGY A+V V
 Sbjct: 833 NESFENTIPFNIFS YTNNSLLKDMINEYFNSINDSKILSLQNKKNTLM DTSGYNAEV RVE 892

Query: 63 DGVELND--KNQFKLTSSANS--KIRVTQNQNIIFNSVFLDFSVSF WIRIPKYKNDGIQN 118
 V+LN FKL SS + K+ VTQN+NI++N++ FS+SF WIRI K+ ++
 Sbjct: 893 GNVQLNP IFPFDFKLGSSGDDRGKIVITQNENIVNAMY EFSISFWIRINKWVSN--- 948

Query: 119 YIHNEYTIINCMKNNSGWKISIRGNRIWTLIDINGKTKSVFFEYNIREDISEYINRWFF 178

tr Q45967 Neurotoxin consisting of botulinum neurotoxin D and C1 1285
Q45967_CLOBO [Clostridium botulinum D] AA align

Score = 206 bits (523), Expect = 1e-51
 Identities = 150/480 (31%), Positives = 239/480 (49%), Gaps = 48/480 (10%)

Query: 3 NKYLKTIMPFDSLITYTNDTILIEFMNKYNSEXXXXXXXXRYKDNNLIDLSGYGAKVEVY 62
 N+ + +PF++ YTN++L +M N+Y + + K N L+D SGY A+V V
 Sbjct: 833 NESFENTIPFNIFSYTNNSSLKDMINEYFNSINDSKILSLQNKKNTLMDSGYNAEV RVE 892

Query: 63 DGVELND--KNQFKLTSSANS--KIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQN 118
 V+LN FKL SS + K+ VTQN+NI++N++ FS+SFWIRI K+ ++
 Sbjct: 893 GNVQLNPPIFPFDLKLGSSGDRGKIIVTQNENIVNAMYESFSISFWIRINKWVS N---- 948

Query: 119 YIHNEYTIINCMKNNSGWKISIRGNRIWTLIDINGKTKSVFFEYNIREDISEYINRWFF 178
 YTI+ +KNNSGW I I N +++TE + + F Y+I ++ + Y N+WFF
 Sbjct: 949 --LPGYTIIDSVKNNSGWSIGIISNFLVFTLKQNENSEQDINF SYDISKNAAGY-NKWF F 1005

Query: 179 VTITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLD-----GDIDRTQFI 228
 VTIT N + N IYINGKL +K++ + + I F+++ D D +
 Sbjct: 1006 VTITTNNMMGNMMIYINGKLIDTIKVKELTGINFSKTITFQMNKIPNTGLITS SDNIN-M 1064

Query: 229 WMKYFSIFNTELSQSNI EERYKI QSYSEYLKDFWGPNPLMYNKEYYM FNAGNKN SYIKL KK 288
 W++ F IF EL +I + Y+ +KD+WGN L Y+KEYYM N N Y+ K
 Sbjct: 1065 WIRDFYIFAKELDDKDINILFNSLQYT NVVKDYWGNDLRYDKEYYMINVN YMNRYSKKG 1124

Query: 289 DSPVGEILTRSKYQNQSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNL 348
 + I+ ++ N N D G K L+R + ND VR E+ +Y +
 Sbjct: 1125 NG----IVFNTRKNNN-----DFNEG YKIIIKRIRG--NTNDTRVRGENVLYFNTTID 1171

Query: 349 NQEWR--VYTXXXXXXXXXXXXXAPISDSDEF--YNTIQIKEYDEQPTYSQOLLFKKDEE 404
 N+++ +Y A D E Y+ I+ + Y+ Q LF
 Sbjct: 1172 NKQYSLGMYKPSRNLGTDLVLGALDQPMDEIRKYGSFIIQPCNTFDYYASQ-LFLSSNA 1230

Query: 405 STDEIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKL---GCNWQFIPKDE 461
 +T+ +G++ I + P+ DY+ ++ + +K + Y L +W F+P E
 Sbjct: 1231 TTNRLGILSIGSY----SFKLGDDYWFNHEYLIPVIKIEHYASLLESTSTHWVFVPA SE 1285

tr Q9LBR1 Neurotoxin [Clostridium botulinum] 1285 AA align
Q9LBR1_CLOBO

Score = 205 bits (522), Expect = 1e-51
 Identities = 149/480 (31%), Positives = 239/480 (49%), Gaps = 48/480 (10%)

Query: 3 NKYLKTIMPFDSLITYTNDTILIEFMNKYNSEXXXXXXXXRYKDNNLIDLSGYGAKVEVY 62
 N+ + +PF++ YTN++L +M N+Y + + K N L+D SGY A+V V
 Sbjct: 833 NESFENTIPFNIFSYTNNSSLKDMINEYFNSINDSKILSLQNKKNTLMDSGYNAEV RVE 892

Query: 63 DGVELND--KNQFKLTSSANS--KIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQN 118
 V+LN FKL SS + K+ VTQN+NI++N++ FS+SFWIRI K+ ++
 Sbjct: 893 GNVQLNPPIFPFDLKLGSSGDRGKIIVTQNENIVNAMYESFSISFWIRINKWVS N---- 948

Query: 119 YIHNEYTIINCMKNNSGWKISIRGNRIWTLIDINGKTKSVFFEYNIREDISEYINRWFF 178

YPIII+ +KNNSGW I I N +++TL + + F X+I ++ + Y N+WFF
 Sbjct: 949 --LPGYTIIDSVKNNSGWSIGIISNFLVFTLKQNENSEQDINFSYDISKNAAGY-NKWFF 1005

 Query: 179 VTITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLD-----GDIDRTQFI 228
 VTIT N + N IYINGKL +K++ + + I F++ D D +
 Sbjct: 1006 VTITTNMMGNMMIYINGKLIDTIKVKELTGINFSKTITFQMNKIPNTGLITSDSDNIN-M 1064

 Query: 229 WMKYFSIFNTELSQSNIIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKK 288
 W++ F IF EL +I + Y+ +KD+WGN L Y+KEYYM N N Y+ K
 Sbjct: 1065 WIRDFYIFAKELDDKDINILFNSLQYTNNVKDYWGNDLRYDKEYYMINVNVMNRYSKKG 1124

 Query: 289 DSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIIRKSNSQSINDDIVRKEDYIYLDFFNL 348
 + I+ ++ N N D G K LI+R + ND VR E+ +Y +
 Sbjct: 1125 NG----IVFNTRKNNN-----DFNEGKIIIKRIRG--NTNDTRVRGENVLYFNTTID 1171

 Query: 349 NQEWR--VYTXXXXXXXXXXXXXAPISDSDEF--YNTIQIKEYDEQPTYSQQLFFKDEE 404
 N+++ +Y A DE Y + I+ + Y+ Q LF
 Sbjct: 1172 NKQYSLGMYKPSRNLGTDLVPLGALDQPMDEIRKYGSFIIQPCNTFDYYASQ-LFLSSNA 1230

 Query: 405 STDEIGLIGIHRFYESGIVFEYKDYFCISKWYLKEVKRKPYNLKL---GCNWQFIPKDE 461
 +T+ +G++ I + F+ DY+ ++ + +K + Y L +W F+P E
 Sbjct: 1231 TTNRLGILSIGSY----SFKLGDDYWFNHEYLIPVIKIEHYASLLESTSTHWVFVPASE 1285

tr Q93N27 **Tetanus toxin (Fragment) [Clostridium tetani]** 1310 AA
Q93N27_CLOTE align

Score = 200 bits (509), Expect = 5e-50
 Identities = 133/430 (30%), Positives = 216/430 (49%), Gaps = 27/430 (6%)

 Query: 46 DNNLI-DLSGYGAKVEVYDGVEL---NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDF 100
 +N++I D+SG+ + V Y +L N K L ++ +S++ V + +I +N +F +P
 Sbjct: 893 NNDIISDISGFNSSVITYPDQLVPGINGK-AIHLVNNESSEVIVHKAMDIEYNDMFNNF 951

 Query: 101 SVSFWRIPKYKNDGIQNYIHNEYTIINCMKN----NSGWKISIRGNRIIWTLIDINGK 155
 +VSFW+R+PK ++ Y NEY+I+ MK SGW +S++GN +IWTL D G+
 Sbjct: 952 TVSFWLVPKVSASHLEQYDTNEYSIISSMKYSLSIGSGWSVSLKGNNLIWTLKDSAGE 1011

 Query: 156 TKSVFFEYNIREDISEYI-NRWFFVTITNN-LNNAKIYINGKLESNTDIKDIREVIANGE 213
 + + F ++ + + Y+ N+W F+TEN+ L++A +YING I + +I + + +
 Sbjct: 1012 VRQITFR-DLSDKFNAYLANKWVFITITNDRLSSANLYINGVLMGSAEITGLGAIREDNN 1070

 Query: 214 IIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIIEERYKIQSYSEYLKDFWGNPLMYNKEYY 273
 I KLD + Q++ + F IF I+ I+ X +L+DFWGNPL Y+ EYX
 Sbjct: 1071 ITLKLDRCNNNNQYVSIDKFRIFCKALNPKEIEKLYTSYLSITFLRDFWGNPLRYDTEYY 1130

 Query: 274 MFNAGNKNSYIKLKKDSPVGIELTRSKYNQNSKYINYRDLYIGEKFIIIRKSNSQSINDD 333
 + + + +LX + + Y I YR LY G EFTI+R + + I D
 Sbjct: 1131 LIPVAYSSKDVQLKNITDYMILTNAPSYTNGKLNIIYRRLYSGLKFIIKRYTPNNEI-DS 1189

 Query: 334 IVRKEDYIYLDFFNLNQEWRVYXXXXXXXXXXAPI---SDSDEFNTIQIKEYDEQ 390
 VR D+I L N E V + + + Y + + + +
 Sbjct: 1190 FVRSGDFIKLYVSNNNEHIVGVYPKDGNAFNNLDRILRVGYNAPGIPLYKKMEAVKRLDL 1249

 Query: 391 PTYSQQLFFKDEESTDEIGLIGIHRFYESGIVFEYKDYFCISKWYLKEVKRKPYNLKL 450
 TYS QI D+ + + + GL+G R I + +D S WY +K K L

Sbjct: 949 YTIII+ +KNNSGW I I N +++Tl + + E Y+I ++ + Y N+WFF
 --LPGYTIIDSVKNNSGWSIGIISNFLVFTLKQNENSEQDINFSYDISKNAAGY-NKWFF 1005

 Query: 179 VTITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLD-----GDIDRTQFI 228
 VTIT N + N IYINGKl +K++ + + I E++ D O +
 Sbjct: 1006 VTITTNNMMGNMMIYINGKLIDTIKVKELTGINFSKTITFQMNKIPNTGLITSDSDNIN-M 1064

 Query: 229 WMKYFSIFNTELSQSNIIEERYKIQSYSEYLKDFWGNPLMYNKEYMFNAGNKNSYIKLKK 288
 W++ F IF EL +I + Y+ +KD+WGN L Y+KEYYM N N Y+ K
 Sbjct: 1065 WIRDFYIFAKELDDKDINILFNSLQYTNVVKDYWGNDLRYDKEYYMINVNVMRYSKKG 1124

 Query: 289 DSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFNL 348
 + I+ ++ N N D G K II+R + ND VR E+ +Y +
 Sbjct: 1125 NG---IVFNTRKNNN-----DFNEGKYKIIKRIRG--NTNDTRVRGENVLYFNTTID 1171

 Query: 349 NQEWR--VYTXXXXXXXXXXXXXAPISDSDEF--YNTIQIKEYDEQPTYSCQLLFFKDEE 404
 N+++ +Y A DE Y+ I+ + Y+ Q LF
 Sbjct: 1172 NKQYSLGMYKPSRNLGTDLVPLGALDQPMDEIRKYGSFIIQPCNTFDYYASQ-LFLSSNA 1230

 Query: 405 STDEIGLIGIHRFYESGIVFEELYKDYFCISKWYLKEVKRKPYNLKL---GCNWQFIPKDE 461
 +T+ +G++ I + Y+ DY+ ++ + +K + Y L +W R+P E
 Sbjct: 1231 TTNRLGILSIGSY----SFKLGDDYWFNHEYLIPVIKIEHYASLLESTSTHWVFVPASE 1285

tr Q93N27 Tetanus toxin (Fragment) [Clostridium tetani] 1310 AA
Q93N27_CLOTE align

Score = 200 bits (509), Expect = 5e-50
 Identities = 133/430 (30%), Positives = 216/430 (49%), Gaps = 27/430 (6%)

Query: 46 DNNLI-DLSGYGAKEVYDGVEL---NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDF 100
 +N++I D+SG+ + V Y +L N K L ++ +S++ V + +I +N +F +P
 Sbjct: 893 NNDIISDISGFNSSVITYPDQLVPGINGK-AIHLVNNESSEVIVHKAMDIEYNDMFNNF 951

 Query: 101 SVSFWRIPKYKNDGIQNYIHNEYTIINCMKN----NSGWKISIRGNRIIWTLIDINGK 155
 +VSEW+R+PK ++ Y NEY+I+ MK SGW +S++GN +IWTL D G+
 Sbjct: 952 TVSFWLVPKVSASHLEQYDTNEYSIISSMKYKSLSIGSGWSVSLKGNNLIWTLKDSAGE 1011

 Query: 156 TKSVFFEYNIREDISEYI-NRWFFVTITNN-LNNAKIYINGKLESNTDIKDIREVIANGE 213
 + + F ++ + + Y+ N+W F+TITN+ L+A +YING L + +I + + +
 Sbjct: 1012 VRQITFR-DLSDKFNAYLANKWVFITITNDRLSSANLYINGVLMGSAEITGLGAIREDNN 1070

 Query: 214 IIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIIEERYKIQSYSEYLKDFWGNPLMYNKEYY 273
 I KLD + Q++ + E IP L+ I+ X +L+DFWGNPL Y+ EYY
 Sbjct: 1071 ITLKLDRCNNNNQYVSIDKFRIIFCKALNPKEIEKLYTSYLSITFLRDFWGNPLRYDTEYY 1130

 Query: 274 MFNAGNKNSYIKLKKDSPVGELTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDD 333
 + + + ++LK + + Y I YR LY G RPII+R + + T D
 Sbjct: 1131 LIPVAYSSKDVQLKNITDYMILTNAPSYTNGKLNIIYRRILYSLGKFIIKRYTPNNEI-DS 1189

 Query: 334 IVRKEDYIYLDFFNLNQEWRVYXXXXXXXXXXAPI---SDSDEFYNTIQIKEYDEQ 390
 VR D+I L N E V + + + Y + + + +
 Sbjct: 1190 FVRSGDFIKLYVSNNNEHIVGYPKDGNAFNNLDRILRVGYNAPGIPLYKKMEAVKRLDL 1249

 Query: 391 PTYSCQLLFFKDEESTDEIGLIGIHRFYESGIVFEELYKDYFCISKWYLKEVKRKPYNLKL 450
 TYS QI D+ + + + GL+G K I + +D S WY +K K L

Sbjct: 1250 KTYSVQLKLYDDKDAS--LGLVGTH---NGQIGNDPNRDILIASNWYFNHLKDK----TL 1300

Query: 451 GCNWQFIPKD 460

C+W F+F D

Sbjct: 1301 TCDWYFVPTD 1310

sp P18640 Botulinum neurotoxin type C1 precursor (EC 3.4.24.69) 1290
 BXCl_CLOBO (BoNT/C1) AA
 (Bontoxilysin C1) [Clostridium botulinum] align

Score = 198 bits (503), Expect = 2e-49

Identities = 127/367 (34%), Positives = 193/367 (51%), Gaps = 35/367 (9%)

Query: 3 NKYLKTIMPFDLSIYTNDTILIEFMNKYNSEXXXXXXXXXRYKDNNLIDLGYGAKVEVY 62
 N + +PF++ YTN+++L ++ N+Y + + + N L+D SGY A+V

Sbjct: 836 NNSFQNTIPFNIFSYTNNSSLKDIINEYFNNINDSKILSLQRKNTLVDTSGYNAEVSEE 895

Query: 63 DGVELND--KNQFKLTSSANS--KIRVTQNQNIIFNSVFLDFSVSFWRIPKYKNDGIQN 118
 V+LN FKL SS K+ V+QN+N+NS++ FS+SFWRIPK+ +

Sbjct: 896 GDVQLNPIFPFDKLGSSGEDRGKVIVTQNENIVYNSMYESFSISFWIRINKWVSN---- 951

Query: 119 YIHNEYTIINCMKNNSGWKISIRGNRIWTLIDINGKTKSVFFEYNIREDISEYINRWFF 178
 Y+I+ +KNNSGW I I N +++TL +S+ F Y+I + Y N+WF

Sbjct: 952 --LPGYTIIDSVKNNSGWSIGIISNFLVFTLKQNEDEQSINFYDISNNAPGY-NKWFF 1008

Query: 179 VTITNN-LNNAKIYINGKLESNTDIKDIRVIANGEIIIFKLD-----GDIDRTQFI 228
 VT+TNN + N KIYINGKL +K++ + + I F+++ D D +

Sbjct: 1009 VTVTNNMMGNMKIYINGKLIDTIKVKELTGINFSKTITFEINKIPDTGLITSDSDNIN-M 1067

Query: 229 WMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFGNPLMYNKEYYMFNAGNKN SYIKLKK 288
 W++F IF EL +I + Y+ +KD+WN L VNKEYYM N N Y+

Sbjct: 1068 WIRDFYIFAKELDGKDINILFNSLQYTNVVKDYWGNDLRYNKEYYMVNIDYLNRMYANS 1127

Query: 289 DSPVGEILTRSKYQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNL 348
 +I+ ++ N N D G X II+R + ND VR D +Y D

Sbjct: 1128 ----RQIVFNTRRRNNN-----DFNEGKIIKKRIRG--NTNDTRVRGGDILYFDMTIN 1174

Query: 349 NQEWRVY 355

N+ + ++

Sbjct: 1175 NKAYNLF 1181

tr Q93HT3 Type C botulinaum neurotoxin [bont/C] [Clostridium] 1291
Q93HT3_CLOBO botulinum AA align

Score = 198 bits (503), Expect = 2e-49

Identities = 127/367 (34%), Positives = 193/367 (51%), Gaps = 35/367 (9%)

Query: 3 NKYLKTIMPFDLSIYTNDTILIEFMNKYNSEXXXXXXXXXRYKDNNLIDLGYGAKVEVY 62
 N + +PF++ YTN+++L ++ N+Y + + + N L+D SGY A+V

Sbjct: 837 NNSFQNTIPFNIFSYTNNSSLKDIINEYFNNINDSKILSLQRKNTLVDTSGYNAEVSEE 895

Query: 63 DGVELND--KNQFKLTSSANS--KIRVTQNQNIIFNSVFLDFSVSFWRIPKYKNDGIQN 118

Sbjct: 1250 KTYSVQLKLYDDKDAS--LGLVGTH---NGQIGNDPNRDILIASNWYFNHLKDK---TL 1300

Query: 451 GCNWQFIPKD 460

C+W F+P P

Sbjct: 1301 TCDWYFVPTD 1310

sp P18640 Botulinum neurotoxin type C1 precursor (EC 3.4.24.69) 1290
BXC1_CLOBO (BoNT/C1) AA
(Bontoxilysin C1) [Clostridium botulinum] align

Score = 198 bits (503), Expect = 2e-49

Identities = 127/367 (34%), Positives = 193/367 (51%), Gaps = 35/367 (9%)

Query: 3 NKYLKTIMPFDLSIYTNDTILIEFMNKYNSEXXXXXXXXXRYKDNNLIDLGYGAKVEVY 62
N + +PF++ YTN+++L ++ N+Y + + + N L+D SGY A+V

Sbjct: 836 NNSFQNTIPFNIFSYTNNSSLKDIINEYFNNINDSKILSLQRKNTLVDTSGYNAEVSEE 895

Query: 63 DGVELND--KNQFKLTSSANS--KIRVTQNQNIIFNSVFLDFSVSFWRIPKYKNDGIQN 118
V+LN EKL SS K+ VHQN+NI++NS++ FS+SFWRIL K+ ++

Sbjct: 896 GDVQLNPPIFPFDLKGSSEDRGKVIVTQNENIVYNSMYESFSISFWIRINKWVSN---- 951

Query: 119 YIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFF 178
YTTI+ +KNNSGW I I N +++TL +S+ F Y+I + Y N+WF

Sbjct: 952 --LPGYTIIDSVKNNSGWSIGIISNFLVFTLQNEDEQSINFSYDISNNAPGY-NKWFF 1008

Query: 179 VTITNN-LNNAKIYINGKLESNTDIKDIRREVIANGEIIFKLD-----GDIDRTQFI 228
VT+TNN + N KIYINGKL +K+ + + I F+++ D D +

Sbjct: 1009 VTVTNMMGMNMKIYINGKLIDTIKVKELTGINFSKTITFEINKIPDTGLITSDSDNIN-M 1067

Query: 229 WMKYFSIFNTELSQSNIERYKIQSYSEYLKDFWGNPLMYNKEYMFNAGNKN SYIKLKK 288
W++ F IF EL +I + Y+ +KD+WGN L YNKEYYM N N Y+

Sbjct: 1068 WIRDFYIIFAKELDGKDINILFNSLQYTNNVKDYWGNDLRYNKEYYMVNIDYLNRYMYANS 1127

Query: 289 DSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNL 348
+T+ + + N N D G M T+R + ND VR D +Y D

Sbjct: 1128 ----RQIVFNTRRRNNN-----DFNEGKIIIKRIRG--NTNDTRVRGGDILYFDMTIN 1174

Query: 349 NQEWRVY 355

N+ + ++

Sbjct: 1175 NKAYNLF 1181

tr Q93HT3 Type C botulinaum neurotoxin [bont/C] [Clostridium] 1291
Q93HT3_CLOBO botulinum AA align

Score = 198 bits (503), Expect = 2e-49

Identities = 127/367 (34%), Positives = 193/367 (51%), Gaps = 35/367 (9%)

Query: 3 NKYLKTIMPFDLSIYTNDTILIEFMNKYNSEXXXXXXXXXRYKDNNLIDLGYGAKVEVY 62
N + +PF++ YTN+++L ++ N+Y + + + N L+D SGY A+V

Sbjct: 837 NNSFQNTIPFNIFSYTNNSSLKDIINEYFNNINDSKILSLQRKNTLVDTSGYNAEVSEE 895

Query: 63 DGVELND--KNQFKLTSSANS--KIRVTQNQNIIFNSVFLDFSVSFWRIPKYKNDGIQN 118

V+LN EKL SS K+ VTQN+NL++NS++ FS+SFWIRI K+ ++
 Sbjct: 897 GDVQLNP1FPFDKLGSSGEDRGKVIVTQNEVIVYNSMYESFSISFWIRINKWVN---- 952

Query: 119 YIHNEYTIINCMKNNSGWKISIRGNRIWTLIDINGKTKSVFFEYNIREDISEYINRWFF 178
 YTTT+ +RNNNSGW I I N +++TL +S+ F Y+I + Y N+WFF

Sbjct: 953 --LPGYTIIDSVKNNSGWSIGIISNFLVFTLKQNEDEQSINSYDISNNAPGY-NKWFF 1009

Query: 179 VTITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLD-----GDIDRTQFI 228
 VT+TNN + N KIYINGKL +K++ + + I F+++
 D D +
 Sbjct: 1010 VTVTNNMMGNMKIYINGKLIDTIKVKELTGINFSKTITFEINKIPDTGLITSDSDNIN-M 1068

Query: 229 WMKYFSIFNTELSQSNIIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKK 288
 W++ F IF EL +I + Y+ +KD+WGN L YNKEYYM N N Y+
 Sbjct: 1069 WIRDFYIFAKELDGKDINILFNSLQYTNVVKDYWGNDLRYNKEYYMVNIDYLNRMYANS 1128

Query: 289 DSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNL 348
 +T+ ++ N N D G K II+R + ND VR D +Y D
 Sbjct: 1129 ----RQIVFNTRRRNNN-----DFNEGKIIKRIRG--NTNDTRVRGGDILYFDMTIN 1175

Query: 349 NQEWRVY 355
 N+ + ++
 Sbjct: 1176 NKAYNLF 1182

tr Q7WUH9 Botulinum neurotoxin type B (Fragment) [bont/B] 78 AA
 Q7WUH9_CLOBO [Clostridium
botulinum] align

Score = 148 bits (374), Expect = 2e-34
 Identities = 71/78 (91%), Positives = 74/78 (94%)

Query: 265 PLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRK 324
 PLMYNKEYYMFNAGNKNSYIKLKKDS VGEILTRSKYNQNS YINYR+LYIGEKFIIRRK
 Sbjct: 1 PLMYNKEYYMFNAGNKNSYIKLKKDSSVGEILTRSKYNQNSNYINRNLYIGEKFIIRRK 60

Query: 325 SNSQSINDDIVRKEDYIY 342
 SNSQSINDDIVR +D ++
 Sbjct: 61 SNSQSINDDIVRNDDRVY 78

tr Q7WRW0 Botulinum neurotoxin type B (Fragment) [bont/B] 78 AA
 Q7WRW0_CLOBO [Clostridium
botulinum] align

Score = 147 bits (370), Expect = 6e-34
 Identities = 70/78 (89%), Positives = 74/78 (94%)

Query: 265 PLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRK 324
 PLMYNKEYYMFNAGNKNSYIKLKKDS VGEILTRSKYNQNS YINYR+LYIGEKFIIRRK
 Sbjct: 1 PLMYNKEYYMFNAGNKNSYIKLKKDSSVGEILTRSKYNQNSNYINRNLYIGEKFIIRRK 60

Query: 325 SNSQSINDDIVRKEDYIY 342
 SNSQSINDDIVR +D ++
 Sbjct: 61 SNSQSINDDIVRNDDRVF 78

V+LN FKL SS K+ VTQN+NI++NS++ FS+FWIRI K+ ++
 Sbjct: 897 GDVQLNPIFPFDKLGSSGEDRGKVIVTQNEIVYNSMYESFSISFWIRINKWVN----- 952

Query: 119 YIHNEYTIINCMKNNSGKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFF 178
 YTTT+ +MMNSGW I I N +++TL +S+ F Y+I + Y N+WFF
 Sbjct: 953 --LPGYTIIDSVKNNSGWSIGIISNFLVFTLKQNEDEQSINSYDISNNAPGY-NKWFF 1009

Query: 179 VTITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLD-----GDIDRTQFI 228
 VT+TNN + N KIYINGKL +K++ + + T F+++ D D +
 Sbjct: 1010 VTVTNNMMGNMKIYINGKLIDTIKVKELTGINFSKTITFEINKIPDTGLITSDSDNIN-M 1068

Query: 229 WMKYFSIFNTELSQSNSIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKK 288
 W++ F IF EL +I + Y+ +KD+WGN L YNKEYYM N N Y+
 Sbjct: 1069 WIRDFYIFAKELDGKDINILFNSLQYTNVVKDYWGNDLRYNKEYYMVNIDYLNRMYANS 1128

Query: 289 DSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNL 348
 +T+ + + N N D G K TT+R + ND VR D +Y D
 Sbjct: 1129 ---RQIVFNTRRRNNN-----DFNEGKYIIIKRIRG--NTNDTRVRGGDILYFDMTIN 1175

Query: 349 NQEWRVY 355
 N+ + ++
 Sbjct: 1176 NKAYNLF 1182

tr Q7WUH9 Botulinum neurotoxin type B (Fragment) [bont/B] 78 AA
 Q7WUH9_CLOBO [Clostridium
 botulinum] align

Score = 148 bits (374), Expect = 2e-34
 Identities = 71/78 (91%), Positives = 74/78 (94%)

Query: 265 PLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRK 324
 PLMYNKEYYMFNAGNKNSYIKLKKDS VGEILTRSKYNQNS YINYR+LYIGEKFIIRRK
 Sbjct: 1 PLMYNKEYYMFNAGNKNSYIKLKKDSSVGEILTRSKYNQNSNYINYRNLYIGEKFIIRRK 60

Query: 325 SNSQSINDDIVRKEDYIY 342
 SNSQSINDDIVR +D +Y
 Sbjct: 61 SNSQSINDDIVRNDDRVY 78

tr Q7WRW0 Botulinum neurotoxin type B (Fragment) [bont/B] 78 AA
 Q7WRW0_CLOBO [Clostridium
 botulinum] align

Score = 147 bits (370), Expect = 6e-34
 Identities = 70/78 (89%), Positives = 74/78 (94%)

Query: 265 PLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRK 324
 PLMYNKEYYMFNAGNKNSYIKLKKDS VGEILTRSKYNQNS YINYR+LYIGEKFIIRRK
 Sbjct: 1 PLMYNKEYYMFNAGNKNSYIKLKKDSSVGEILTRSKYNQNSNYINYRNLYIGEKFIIRRK 60

Query: 325 SNSQSINDDIVRKEDYIY 342
 SNSQSINDDIVR +D ++
 Sbjct: 61 SNSQSINDDIVRNDDRVF 78

tr Q6Q799 Non-proteolytic neurotoxin type B (Fragment) [Clostridium] 77 AA
Q6Q799_CLOBO botulinum

align

Score = 146 bits (368), Expect = 1e-33
 Identities = 71/77 (92%), Positives = 73/77 (94%)

Query: 265 PLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLIGEKFIRRK 324

PLMYNKEYYMFNAGNKNSYIKL KDS VGETIL RSKYNQNS YINYR+LYIGEKFIERR+

Sbjct: 1 PLMYNKEYYMFNAGNKNSYIKLVKDSSVGEILRSKYNQNSNYINYRNLYIGEKFIRRE 60

Query: 325 SNSQSINDDIVRKEDYI 341

SNSQSINDDIVRKEDYI

Sbjct: 61 SNSQSINDDIVRKEDYI 77

tr Q79AH9 Botulinum neurotoxin type F (Fragment) [BoNT/F] 366
Q79AH9_CLOBO [Clostridium
botulinum]

AA
align

Score = 142 bits (359), Expect = 1e-32
 Identities = 72/161 (44%), Positives = 104/161 (63%), Gaps = 6/161 (3%)

Query: 6 LKTIMPFDLSIYTNDTILIEFMNKYNSEXXXXXXXXRYKDNNNLIDLGYGAKVEVYDGV 65

L +PF+LS YTND ILI FNK + RY++N ID+SGYG+ + + V

Sbjct: 204 LNNSIPFELSSYTNDKILILYFNKLYKKIKDNSILDMDRYENNKFIDISGYGSNISINGDV 263

Query: 66 EL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNE 123

+ ++NQF + CS S++ + QN +T+N + +FS+SFW+RIPKY N + +NE

Sbjct: 264 YIYSTNRNQFGIYSSKPSEVNIAQNNDIYNGRYQNFISFWVRIPKYFN---KVNLNNE 320

Query: 124 YTIINC MK-NNSGWKISIRGNRIIWTLIDINGKTKSVFFEY 163

YTI+ +C++ NNSGWKIS+ N+IWTL D G + + F Y

Sbjct: 321 YTIIDCIRNNNSGWKISLN YN KIIWTLQDTAGNNQKLVFNY 361

tr Q45861 Botulinum neurotoxin type E (Fragment) [BoNT/E] 367
Q45861_CLOBO [Clostridium
botulinum]

AA
align

Score = 133 bits (335), Expect = 7e-30
 Identities = 68/166 (40%), Positives = 99/166 (58%), Gaps = 5/166 (3%)

Query: 1 MANKYLKTIMPFDLSIYTNDTILIEFMNKYNSEXXXXXXXXRYKDNNNLIDLGYGAKVE 60

M L +PF LS YT+D ILI FNK+ RYK++ +D SGY + +

Sbjct: 199 MVTDTLNNSIPFKLSSYTDDKILISYFNKFFKRIKSSSVLNMRYKNDKYVDTSGYDSNIN 258

Query: 61 VYDGVEL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQN 118

+ V +KNQF + + S++ ++QN II+++ + +FS+SFW+RIP Y N +

Sbjct: 259 INGDVYKYPTNKNQFGIYNDKLSEVNISQNDYIIYDNKYKNFSISFWVRIPNYDNKIVN- 317

Query: 119 YIHNEYTIINC MK-NNSGWKISIRGNRIIWTLIDINGKTKSVFFEY 163

+ +NEXTYIIINC+ NNSGWKIS+ N IWTL D G + + F Y

Sbjct: 318 -VNNEYTIINC MRDNNSGWKVSLNHNEIIWTLQDNAGINQKLA FNY 362

tr Q6Q799 Non-proteolytic neurotoxin type B (Fragment) [Clostridium 77 AA
Q6Q799_CLOBO botulinum]

align

Score = 146 bits (368), Expect = 1e-33
 Identities = 71/77 (92%), Positives = 73/77 (94%)

Query: 265 PLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIRRK 324

PLMYNKEYYMFNAGNKNSYIKL KDS VGETIL RSKYNQNS YINYR+LYIGEKFIRRK+

Sbjct: 1 PLMYNKEYYMFNAGNKNSYIKLVKDSSVGEILRSKYNQNSNYINYRNLYIGEKFIRRE 60

Query: 325 SNSQSINDDIVRKEDYI 341

SNSQSINDDIVRKEDYI

Sbjct: 61 SNSQSINDDIVRKEDYI 77

tr Q79AH9 Botulinum neurotoxin type F (Fragment) [BoNT/F] 366
Q79AH9_CLOBO [Clostridium
 botulinum]

AA
align

Score = 142 bits (359), Expect = 1e-32

Identities = 72/161 (44%), Positives = 104/161 (63%), Gaps = 6/161 (3%)

Query: 6 LKTIMPFDLSIYTNDTILIEFMNKYNSEXXXXXXXXRYKDNNNLIDLSGYGAKVEVYDGV 65

L +PF+LS YTND ILL FNK + RY++N ID+SGYG+ ++ V

Sbjct: 204 LNNSIPFELSSYTNDKILILYFNKLYKKIKDNSILDMDRYENNKFIDISGYGSNISINGDV 263

Query: 66 EL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNE 123

+ ++NQF + SS S++ + QN +T+N + +FS+SFW+RIPKY N + ++ME

Sbjct: 264 YIYSTNRNQFGIYSSKPSEVNIAQNNDIIYNGRYQNFISFWVRIPKYFN---KVNLNNE 320

Query: 124 YTIINC MK-NNSGWKISIRGNRIIWTLIDINGKTKSVFFEY 163

YTIKI+C++ NN SGWKIS+ N+IWTL D G + + F Y

Sbjct: 321 YTIIDCIRNNNSGWKISLN YN KIIWTLQDTAGNNQKLVFNY 361

tr Q45861 Botulinum neurotoxin type E (Fragment) [BoNT/E] 367
Q45861_CLOBO [Clostridium
 botulinum]

AA
align

Score = 133 bits (335), Expect = 7e-30

Identities = 68/166 (40%), Positives = 99/166 (58%), Gaps = 5/166 (3%)

Query: 1 MANKYLKTIMPFDLSIYTNDTILIEFMNKYNSEXXXXXXXXRYKDNNNLIDLSGYGAKVE 60

M L +FF LS YT+D ILL FNK+ RYK++ +D SGY + +

Sbjct: 199 MVTDTLNNSIPFKLSSYTDDKILISYFNKFFKRIKSSSVLNMRYKNDKYVDTSGYDSNIN 258

Query: 61 VYDGVEL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQN 118

+ V +KNQF + + S++ ++QN II+++ + +FS+SFW+RIP Y N +

Sbjct: 259 INGDVYKYPTNKNQFGIYNDKLSEVNISQNDYIIYDNKYKNFSISFWVRIPNYDNKIVN- 317

Query: 119 YIHNEYTIINC MK-NNSGWKISIRGNRIIWTLIDINGKTKSVFFEY 163

+ +NEXTYIIINC MK- NN SGWKIS+ N+IWTL D G + + F Y

Sbjct: 318 -VNNEYTIINC MRDNNSGWKVSLNHNEIIWTLQDNAGINQKLAFNY 362

tr 006018 NTNH protein [NTNH] [Clostridium botulinum] 1198 AA
006018_CLOBO align

Score = 85.5 bits (210), Expect = 2e-15
 Identities = 79/347 (22%), Positives = 145/347 (41%), Gaps = 63/347 (18%)

Query: 51 DLSGYGAKVEVYDGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPK 110
 D+SG V+ D ++I+ V + NI N + FS+ FW+R
 Sbjct: 853 DISGKDTLVQYSIDTLDLKVNGDALYLKEPNQSVNFSNNIFENGLTNSFSICFWLR--- 909

Query: 111 YKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDIS 170
 NG N N +I + NN GW+I N ++++++D NG K+++ + + +S
 Sbjct: 910 --NLGQDNLSSN--LIGNIVNNCGWQIYFENNGLVFSMVDNGNEKNIY---LSDVLS 960

Query: 171 EYINRWFFVTITNN--LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFI 228
 +Y W++++++ + N I+IN KL N I+ I + ++ I + + + I
 Sbjct: 961 KY---WYYISVSVDRLRNKLIFINDKLIVNESIEQILNIYSSNIISL---VNENNPI 1012

Query: 229 WMKYFSIFNTELSQSNIIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFN-----A 277
 ++ SI N L+ + X + Y++D +G L YNK X ++N
 Sbjct: 1013 CIEELSLINKALTSEEVLNSYFTNLNNSYIRD SYGARLEYNKNEYLYNYVFPENS LYEV 1072

Query: 278 GNKNSYIKLKKDSPVGEILTRSKY---NQNSKYI-----NYRDLYIGEKF 319
 N N Y+ +K + + K + ++ +Y+ Y D+ G
 Sbjct: 1073 ENNNMYLSIKNIKNTNILGAKFKLINTDESKQYVQKWDEVICVLGDETEKYADIQAGNNR 1132

Query: 320 I--IRRKSNSQSI--NDDIVR-----KEDYIYLDFFNLNQEWRV 354
 I + K N++ I N++I R ?+ L N N W +
 Sbjct: 1133 IQLVNSKDNARKIIVNNNIFRPNCVLFSYNNKYLSSLRNRNWNMI 1179

tr Q45888 Nontoxic-hemagglutinin [nontoxic-hemagglutinin] 1197
Q45888_CLOBO [Clostridium botulinum] AA
align

Score = 77.4 bits (189), Expect = 6e-13
 Identities = 83/386 (21%), Positives = 159/386 (40%), Gaps = 71/386 (18%)

Query: 16 IYTNDTILIEMFNKNYNSXXXXXXXXXRYKDNNLI--DLSGYGAKVEVYDGVELNDKNQF 73
 + T++P LI K S +DNN + D+SG V+ D + L
 Sbjct: 819 LITSETDLI----KEEKESDYNLFLLTLQEDNNKVIEDISGKNTLVKYSDSISL VYVGNG 874

Query: 74 KLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPK YKNDGIQNYIHNEYTIINCMKNN 133
 V+ + + N + FS+ FW+R N G ++ I ++ +I + +N
 Sbjct: 875 DALYLKEPNESVFSNKVFENGLTNSFSICFWLR---NLG-EDIITSK--LIENKADN 926

Query: 134 SGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINR-WFFVTITNNL--NNAKI 190
 GW+I N ++++++D NG +++ +S+ I++ W++ +I+ + N I
 Sbjct: 927 CGWEIYFENNGLVFSIVDCNGNEENIY-----LSDVISKNWYYISISIDRLRNQLLI 978

Query: 191 YINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIIEERYK 250
 +IN KI +N I+ I + ++ I + + I + + SI N ++ * Y
 Sbjct: 979 FINDKLIANQSIEQILNIYSSSTISL---VNENNPIYVEGLSILNRSITSEEVNNYF 1033

tr 006018 NTNH protein [NTNH] [Clostridium botulinum] 1198 AA
 006018_CLOBO

Score = 85.5 bits (210), Expect = 2e-15
 Identities = 79/347 (22%), Positives = 145/347 (41%), Gaps = 63/347 (18%)

Query: 51 DLSGYGAKVEVYDGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVFWIRIPK 110
 D+SG V+ D ++L+ V + NI N + FS+ FW+R
 Sbjct: 853 DISGKDTLVQYSQTSIDLSYGVNGDALYLKEPNQSVNFSNNIFENGTLNSFSICFWLR--- 909

Query: 111 YKNDGIQNYIHNNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDIS 170
 N G N N +T + NN GW+I N ++++++D NG K+++ + + +S
 Sbjct: 910 --NLGQDNLSSN--LIGNIVNNCGWQIYFENNGLVSMDNCNGNEKNIY---LSDVLS 960

Query: 171 EYINRWFFFVTITNN--LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFI 228
 +Y W++++++ + N I+IN KL N I+ I + * I + + I
 Sbjct: 961 KY---WYYISVSVDRLRNKLLIFINDKLIVNESIEQILNIYSSNIISL---VNENNPI 1012

Query: 229 WMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFN-----A 277
 ++ SI N L+ + X + Y++D +G L YNK X ++N
 Sbjct: 1013 CIEELSILNKALTSEEVLNSYFTNLNNSYIRD SYGARLEYNK NYEL NYVFPENS LYEV 1072

Query: 278 GNKNSYIKLKKDSPVGEILTRSKY---NQNSKYI-----NYRDLYIGEKF 319
 N N Y+ +K + + K +++ +Y+ Y D+ G
 Sbjct: 1073 ENNNMYLSIKNIKNTNILGAKFKLINTDESKQYVQKWDEVIICVLGDTEKYADIQAGNNR 1132

Query: 320 I--IRRKSNSQSI--NDDIVR-----KEDYIYLDFFNLNQEWRV 354
 I + K N++ T N++T R Y+ L N N W +
 Sbjct: 1133 IQLVNSKDNARKIIIVNNNIFRPNCVLFSYNNKYLSSLRNRNWNMI 1179

tr	<u>Q45888</u>	Nontoxic-hemagglutinin [nontoxic-hemagglutinin]	1197
	<u>Q45888_CLOBO</u>	[Clostridium	AA
		botulinum]	<u>align</u>
Score = 77.4 bits (189), Expect = 6e-13			
Identities = 83/386 (21%), Positives = 159/386 (40%), Gaps = 71/386 (18%)			
Query:	16	IYTNDTILIEFMNKYNSEXXXXXXXXXRYKDNNLI--DLSGYGAKVEVYDGVELNDKNQF	73
		+ T++P LI K S +DNN + D+SG V+ D + L	
Sbjct:	819	LITSETDLI---KEEKESDYNLFLLTLQEDNNKVIEDISGKNTLVKYSDSISLVGVNG	874
Query:	74	KLTSSANSKIRVTQNQNIIFNSVFLDFSVSWIRIPKYKNDGIQNYIHNEYTTIINCMKNN	133
		V+ + + N + FS+ FW+R N G ++ I ++ +I +N	
Sbjct:	875	DALYLKEPNESVSFSNKVFENGLTNSFSICFWLR----NLG-EDIITSK--LIENKADN	926
Query:	134	SGWKISIRGNRIIWTLIDINGKTKSFFEYNIREDISEYINR-WFFVTITNNL--NNAKI	190
		GW+I N ++++++D NG +++++ +S+ I++ W++++I+ + N I	
Sbjct:	927	CGWEIYFENNGLVSIVDCNGNEENIY-----LSDVISKNWYYISISIDRLRNQLLI	978
Query:	191	YINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSНИEERYK	250
		+IN KL +N I+ I + ++ I + + I+++ SI N ++ + Y	
Sbjct:	979	FINDKLIANOSIEOILNIYSSSTISL-----VNENNPIYVEGLSILNRSITSEEVNNYF	1033

Query: 251 IQSYSEYLKDWFGNPLMYNKEYYMFN-----AGNKNSYIKLKKDSPV---GEIL 296
 + Y++D G L YNK Y ++N N N Y+ +K + + G
 Sbjct: 1034 SYLNNSYIRDISGERLEYNKIYELYNYVFPENSLYEVTENNNIYLSIKDTNDLNIQGAKF 1093

Query: 297 TRSKYNQNSKYINYRD-----LYIGEKFIIIRRKSNSQ-----SINDDIVR- 336
 + N +Y+ D L EK++ N++ N+DT +
 Sbjct: 1094 KLINIDTNKQYVQKWDGGVVCLLGDEEKYVDISSENNRIQLVSSRDTAKKIIFNNDIFKP 1153

Query: 337 -----KEDYIYLDFFNLNQEWRVY 355
 Y+ L F + N W +Y
 Sbjct: 1154 NCLTFAYNNKYLSSLFRDRNYNWMIY 1179

sp P46082 Botulinum neurotoxin type E, nontoxic component [ent-120] 1162 AA
 BXEN_CLOBO [Clostridium botulinum]
align

Score = 74.7 bits (182), Expect = 4e-12
 Identities = 70/286 (24%), Positives = 129/286 (44%), Gaps = 39/286 (13%)

Query: 45 KDNNLI-DLSGYGAKVEVYDGVELN---DKNQFKLTSSANSKIRVTQNQNIIFNSVFLDF 100
 +DNNN+I D SG VE + L + N LT AN I+ T + N + +F
 Sbjct: 810 QDNNVIGDTSGKNTLVEYPKDIGLVLVYGINNNAIHLTG-ANQNIKFTNDY--FENGLTNNF 866

Query: 101 SVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVF 160
 S+ FW+R K ON I ++ +I ++N GW+I + +++ +ID NG K+++
 Sbjct: 867 SIYFWLRNLK-----QNTIKSK--LIGSKEDNCGWEIYFENDGLVFNIIDSNGNEKNIY 918

Query: 161 FEYNIREDISEYINRWFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDG 220
 +IS + ++T + I+I+ L +N DIK+T + ++ I D
 Sbjct: 919 L-----SNISNKSWHYIVVISINRLKDQLLIFIDNILVANEDIKEILNIYSSDIISLLSDN 973

Query: 221 DIDRTQFIWMKYFSIFNTELSQSNIIEERYKIQSYSEYLKDWFGNPLMYNKEYYMFN--- 276
 + +++++ S+ N ++ + T ? + Y+++F L YN+ Y +F
 Sbjct: 974 N-----NVYIEGLSVLNKTINSNEILTDYFSDLNNSYIRNFDEEILQYNRTYELFNYVFP 1028

Query: 277 -----AGNKNSYIKLKKDSPVGEILTRSKY---NQNSKYINYRD 312
 N N Y+ + ++ + + K N N +Y+ D
 Sbjct: 1029 EIAINKIEQNNNIYLSINNENNLFKPLKFLLNTNPNKQYVQKWD 1074

tr Q9LBS8 NTNHA [ntnha] [Clostridium botulinum] 1196 AA
align

Score = 74.7 bits (182), Expect = 4e-12
 Identities = 61/261 (23%), Positives = 115/261 (43%), Gaps = 38/261 (14%)

Query: 43 RYKDNLI-DLSGYGAKVEVYDGVEL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLD 99
 R + +N+I D+SG + + VEL + S N + + N N + +
 Sbjct: 843 RGPNSNIIIEDISGKNTLIQYTESVELVYGVNGESLYLKSPNETVEFSNN--FFTNGLTNN 900

Query: 100 FSVFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSV 159
 F++ FW+R K+D I N+ NN GW+I N + + +ID NG +SV
 Sbjct: 901 FTICFWLRFTG-KDDDKTRLIGNKV-----NNCGWEIYFEDGLVFEIIDSNGNQESV 952

Query: 251 IQSYSEYLKDFWGNPLMYNKEYYMFN-----AGNKNSYIKLKKDSPV---GEIL 296
 + Y+D G L YNK Y ++N N N Y+ +K + + G
 Sbjct: 1034 SYLNNSYIRDISGERLEYNKIYELYNYVFPENSLYEVTENNIYLSIKDTNDLNIQGAKF 1093

Query: 297 TRSKYNQNSKYINYRD-----LYIGEKFIIRRKSNSQ-----SINDDIVR- 336
 + N +Y+ D L EK++ N++ M+DT +
 Sbjct: 1094 KLINIDTNKQYVQWKDEGVVCLLGDEEKYVDISSENNRIQLVSSRDTAKKIIIFNNNDIFKP 1153

Query: 337 -----KEDYIYLDFFNLNQEWRVY 355
 Y+ L F + N W +Y
 Sbjct: 1154 NCLTFAYNNKYLSSLFRDRNWNMIY 1179

sp P46082 Botulinum neurotoxin type E, nontoxic component [ent-120] 1162 AA
 BXEN_CLOBO [Clostridium botulinum]
align

Score = 74.7 bits (182), Expect = 4e-12
 Identities = 70/286 (24%), Positives = 129/286 (44%), Gaps = 39/286 (13%)

Query: 45 KDNNLI-DLSGYGAKVEVYDGVELN--DKNQFKLTSSANSKIRVTQNQNIIFNSVFLDF 100
 +IENN+I D SG VE + L + N LT AN I+ T + N + +F
 Sbjct: 810 QDNNVIGDTSGKNTLVEYPKDIGLVYGINNNAIHTG-ANQNIKFTNDY--FENGLTNNF 866

Query: 101 SVSFWRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVF 160
 S+ FW+R K QN I ++ +I ++N GW+I + +++ +ID NG K+++
 Sbjct: 867 SIYFWLRNLK-----QNTIKSK--LIGSKEDNCGWEIYFENDGLVFNIIDSNGNEKNIY 918

Query: 161 FEYNIREDISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDG 220
 +IS + ++T + I+I+ L +N DIK+T + ++ I D
 Sbjct: 919 L-----SNISNKSWHYIVVISINRLKDQLLIFIDNILVANEDIKEILNIYSSDIISLLSDN 973

Query: 221 DIDRTQFIWMKYSI芬TELSQSNIIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFN--- 276
 + + + + S+ N ++ + I Y + Y++F L YN+ Y +FN
 Sbjct: 974 N-----NVYIEGLSVLNKTINSNEILTDYFSDLNNSYIRNFDEEILQYNRTYELFNYVFP 1028

Query: 277 -----AGNKNSYIKLKKDSPVGEILTRSKY---NQNSKYINYRD 312
 N N Y+ + ++ + + K N N +Y+ D
 Sbjct: 1029 EIAINKIEQNNNIYLSINNENNLFKPLKFKLNTNPNKQYVQKWD 1074

tr Q9LBS8 NTNHA [ntnha] [Clostridium botulinum] 1196 AA
 Q9LBS8_CLOBO
align

Score = 74.7 bits (182), Expect = 4e-12
 Identities = 61/261 (23%), Positives = 115/261 (43%), Gaps = 38/261 (14%)

Query: 43 RYKDNNLI-DLSGYGAKVEVYDGVEL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLD 99
 R + +N+I D+SG ++ + VEL + S N + + N N + +
 Sbjct: 843 RGPNSNIIIEDISGKNTLIQYTESVELVYGVNGESLYLKSPNETVEFSNN--FFTNGLTNN 900

Query: 100 FSVSFWRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSV 159
 F++ FW+R K+D I N+ NN GW+I N + + + ID NG +SV
 Sbjct: 901 FTICFWLRFTG-KDDDKTRLIGNKV-----NNCGWEIYFEDNGLVFEIIDSNGNQESV 952

Query: 160 FFEYNIREDISEYINRWFFVTIT--NNLNNAKIYINGKLESNTDIKDIREVIANGEIIFK 217
 + I N W+++T+ + + I+IN K +N I+ I + + I
 Sbjct: 953 YLSNVIN-----NNWYYISISVDRSKDQLLIFINDKNVANVSIEQILNIYSTNVISL- 1004

Query: 218 LDG DIDRTQFIWMKYFSIFNTELSQSNEERYKIQSYSEYLKDFWGNPLMYNKEYYMFN- 276
 +++ I+++ S+ + ++ + X + Y++D + L YNK Y ++N
 Sbjct: 1005 ----VNKNNSIYVEELSVLDKTVTSEEVIRNYFSYLDNSYIRDSSKSLEYNKNYQLYNY 1060

Query: 277 -----AGNKNSYIKLK 287
 N SY+ LK
 Sbjct: 1061 VFPKTSLYEVNDNNKSYLSLK 1081

sp Q06366 Botulinum neurotoxin type E, nontoxic component 1162
 BXEN_CLOBU [Clostridium AA
 butyricum] align

Score = 74.3 bits (181), Expect = 5e-12
 Identities = 62/236 (26%), Positives = 112/236 (47%), Gaps = 25/236 (10%)

Query: 45 KDNNLIDLSGYGAKVEVYDGVELN---DKNQFKLTSSANSKIRVTQNQNIIFNSVFLDF 100
 +DNN+I D SG VE + L + N LT AN I+ T + N + +F
 Sbjct: 810 QDNNVIGDTSGKNTLVEYPKDIGLVYGINNNAIHTG-ANQNIKFTNDY--FENGLTNNF 866

Query: 101 SVSFWRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVF 160
 S+ FW+R QN I ++ +I ++N GW+I N +++ +ID NG K+++
 Sbjct: 867 SIYFWLRNLN-----QNTIKSK--LIGSKEDNCWEIYFENNGL VFNIIDSNGNEKNIY 918

Query: 161 FEYNIREDISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDG 220
 +IS + ++T + I+I+ L +N DIK+T + ++ I D
 Sbjct: 919 L-----SNISNKSWHYIVVISINRLKDQLLIFIDNIVANEDIKEILNIYSSDIISLLSDN 973

Query: 221 DIDRTQFIWMKYFSIFNTELSQSNEERYKIQSYSEYLKDFWGNPLMYNKEYYMFN 276
 + + + + S+ N ++ + I Y + Y++F L YN+ Y +YN
 Sbjct: 974 N-----NVYIEGLSVLNKTINSNEILTDYFSDLNNSYIRNFDEEILQYNRTYELFN 1024

tr Q9ZAJ9 Ntnh protein [ntnh] [Clostridium 1197 AA
Q9ZAJ9_CLOBO botulinum] align

Score = 74.3 bits (181), Expect = 5e-12
 Identities = 66/288 (22%), Positives = 127/288 (43%), Gaps = 41/288 (14%)

Query: 16 IYTNDTILIEFMNKYNSEXXXXXXXXXRYKDNNLI--DLSGYGAKVEVYDGVELNDKNQF 73
 + T++T LI K E +DNN + D+SG V+ D + L
 Sbjct: 819 LITSETDLI----KEEKESDYNLFIFTLQEDNNKVIEDISGKNTLVKYSDSISLVYGVNG 874

Query: 74 KLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWRIPKYKNDGIQNYIHNEYTIINCMKNN 133
 V+ + N + FS+ FW+R N G ++ I ++ +I +N
 Sbjct: 875 DALYLKEPDESFSNKAFENGLTNSFSICFWLR----NLG-EDIITSK--LIENKADN 926

Query: 134 SGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINR-WFFVTITNNL--NNAKI 190
 GW+I N ++++ +D NG +++++ +S+ I++ W++ +I+ + N I
 Sbjct: 927 CGWEIYFENGLVFSIVDCNGNEENIY-----LSDVISKNWYYISISIDRLRNQLLI 978

Query: 160 FFEYNIREDISEYINRWFFVTIT--NNLNNNAKIYINGKLESNTDIKDIREVIANGEIIFK 217
 + I N W+++I+ + + I+IN K +N I+ I + + I
 Sbjct: 953 YLSNVIN-----NNWYYISISVDRSKDQLLIFINDKNVANVSIEQILNIYSTNVISL- 1004

Query: 218 LDG DIDRTQFIWMKYFSIFNTELSQSNSIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFN- 276
 +++ I+++ S+ + ++ + X + X++D + L YN+ Y ++N
 Sbjct: 1005 ---VNKNNSIYVEELSVLDKTVTSEEVIRNYFSYLDNSYIRDSSKSLLNEYNKNYQLNY 1060

Query: 277 -----AGNKNSYIKLK 287
 N SY+ LK
 Sbjct: 1061 VFPKTSLYEVNDNNNSYLSLK 1081

sp Q06366 Botulinum neurotoxin type E, nontoxic component 1162
 BXEN_CLOBU [Clostridium AA
 butyricum] align

Score = 74.3 bits (181), Expect = 5e-12
 Identities = 62/236 (26%), Positives = 112/236 (47%), Gaps = 25/236 (10%)

Query: 45 KDNNLIDLSGYGAKVEVYDGVELN--DKNQFKLTSSANSKIRVTQNQNIIFNSVFLDF 100
 +IENN+I D SG VE + L + N LT AN I+ T + N + +F
 Sbjct: 810 QDNNVIGDTSGKNTLVEYPKDIGLVYGINNNAIHTG-ANQNIKFTNDY--FENGLTNNF 866

Query: 101 SVSFWRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVF 160
 S+ FW+R QN I ++ +I ++N GW+I N +++ +ID NG K+++
 Sbjct: 867 SIYFWLRNLN----QNTIKSK--LIGSKEDNCWEIYFENNGL VFNIIDSNGNEKNIY 918

Query: 161 FEYNIREDISYEYINRWFFVTITNNLNNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDG 220
 +I.S + ++T + I+I+ L +N DIK+I + ++ I D
 Sbjct: 919 L----SNISNKSWHYIVVISINRLKDQLLIFIDNIVANEDIKEILNIYSSDIISLLSDN 973

Query: 221 DIDRTQFIWMKYFSIFNTELSQSNSIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFN 276
 + + + + S+ N ++ + I Y + Y+++F L YN+ Y +FN
 Sbjct: 974 N----NVYIEGLSVLNKTINSNEILTDYFSDLNNSYIRNFDEEILQYRNRTYELFN 1024

tr Q9ZAJ9 Ntnh protein [ntnh] [Clostridium 1197 AA
 Q9ZAJ9_CLOBO botulinum] align

Score = 74.3 bits (181), Expect = 5e-12
 Identities = 66/288 (22%), Positives = 127/288 (43%), Gaps = 41/288 (14%)

Query: 16 IYTNDTILIEFMNKYNSEXXXXXXXXXRYKDNNLI--DL SGY GAKVEVYDGVELNDKNQF 73
 + T++T LI K E +DNN + D+SG V+ D + L
 Sbjct: 819 LITSETDLI----KEEKESDYNLFIFTLQEDNNKVIEDISGKNTLVKYSDSISL VYGVNG 874

Query: 74 KLTSSANSKIRVTQNQNIIFNSVFLDFSFSFWIRIPKYKNDGIQNYIHNEYTIINCMKNN 133
 V+ + N + FS+ FW+R N G ++ I ++ +I +N
 Sbjct: 875 DALYLKEPDESFSNKAFENGTLNSFSICFWL-----NLG-EDIITSK--LIENKADN 926

Query: 134 SGWKISIRGNRIIWTLIDINGKTKSFFEYNIREDISYEYINR-WFFVTITNNL--NNAKI 190
 GW+I N ++++D NG +++++ +S+ I++ W+ + +I+ + N I
 Sbjct: 927 CGWEIYFENNGL VFSIVDCNGNEENIY-----LSDVISKWYYISISIDRLRNQLLI 978

Query: 191 YINGKLESNTDIKDIREVIANGEIIIFKLDGIDRTQFIWMKYFSIFNTELSQSNEERYK 250
 +IN KL +N I+ I + ++ I + + I++ ST N ++ + Y
 Sbjct: 979 FINDKLIANQSIEQILNIYSSNTISL----VNENNPIYIEGLSILNRSITSEEVNNYF 1033

Query: 251 IQSYSEYLKDWFGNPLMYNKEYYMFN-----AGNKNSYIKLK 287
 + Y++D G L YNK Y ++N N N Y+ +K
 Sbjct: 1034 SYLNNSYIRDISGERLEYNKTYELYNYVFPENSPLYEVTEENNIYLSIK 1081

tr P71117 Nontoxic-nonhemagglutinin [nontoxic-nonhemagglutinin] 1197
P71117_CLOBO [Clostridium AA
 botulinum] align

Score = 74.3 bits (181), Expect = 5e-12
 Identities = 66/288 (22%), Positives = 127/288 (43%), Gaps = 41/288 (14%)

Query: 16 IYTNDTILIEMFNKYNSEXXXXXXXXXRYKDNNLI--DL SGY GAKVEVYDGVELNDKNQF 73
 + T++T LI K E +DNN + D+SG V+ D + L
 Sbjct: 819 LITSETDLI---KEEKESDYNLFLFTLQEDNNKVIEDISGKNTLVKYSDSISL VYGVNG 874

Query: 74 KLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNN 133
 V+ * N + FS+ FW+R N G ++ I ++ +I +N
 Sbjct: 875 DALYLKEPDESVSFSNKAFENGTLNSFSICFWLR----NLG-EDIITSK--LIENKADN 926

Query: 134 SGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINR-WFFVTITNNL--NNAKI 190
 CW+I N ++++++D NG +++++ +S+ I++ W++++T+ + N I
 Sbjct: 927 CGWEIYFENNGLVLFSIVDCNGNEENIY-----LSDVISKNWYYISISIDRLRNQLLI 978

Query: 191 YINGKLESNTDIKDIREVIANGEIIIFKLDGIDRTQFIWMKYFSIFNTELSQSNEERYK 250
 +IN KL +N I+ I + ++ I + + I++ ST N ++ + Y
 Sbjct: 979 FINDKLIANQSIEQILNIYSSNTISL----VNENNPIYIEGLSILNRSITSEEVNNYF 1033

Query: 251 IQSYSEYLKDWFGNPLMYNKEYYMFN-----AGNKNSYIKLK 287
 + Y++D G L YNK Y ++N N N Y+ +K
 Sbjct: 1034 SYLNNSYIRDISGERLEYNKTYELYNYVFPENSPLYEVTEENNIYLSIK 1081

tr O87710 NTN H protein [ntnh] [Clostridium baratii] 1160 AA
O87710_9CLOT align

Score = 74.3 bits (181), Expect = 5e-12
 Identities = 87/357 (24%), Positives = 157/357 (43%), Gaps = 50/357 (14%)

Query: 6 LKTIMPFDLSIYTNDTILIE----MFNKNY-----SEXXXXXXXRYKDNNLI-DLS 53
 L+ IM L+ D + IE + FN Y S + +D N+E D S
 Sbjct: 759 LQLIMQNSLNSLNFDFLDIEKIKCLFNSYTRLLIKKQSSPYELSLYAFQGEDKNVIGDGS 818

Query: 54 GYGAKVEVYDGVEL--NDKNQFKLTSSANSKIRVTQN--QNIIFNSVFLDFSVSFWIRIP 109
 G VE + + L N + +N + T + +N + NS FS+ FW+R
 Sbjct: 819 GKNTLVEYTNDIGLIYGINNNALYLNQSNQSVSFTNDYFENGLTNS----FSIYFWLR-- 872

Query: 110 KYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDI 169
 D I++ +I+ +N CW+I + N +++ +ED NG K ++ I
 Sbjct: 873 NLGKDIKS-----KLISSKLDNCGWEIYLEDNGLVFNIIDSNGSYKKIY-----I 918

Query: 191 YINGKLESNTDIKDIRREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIIEERYK 250
 +IN KL +N I+ I + ++ I + + I++ ST N ++ + Y
 Sbjct: 979 FINDKLIAQSIEQILNIYSSNTISL----VNENNPIYIEGLSILNRSITSEEVNNYF 1033

Query: 251 IQSYSEYLKDWFGNPLMYNKEYYMFN-----AGNKNSYIKLK 287
 + Y++D G L YNK Y ++N N N Y+ +K
 Sbjct: 1034 SYLNNSYIRDISGERLEYNKTYELYNYVFPENSLYEVTENNIYLSIK 1081

tr P71117 **Nontoxic-nonhemagglutinin [nontoxic-nonhemagglutinin]** 1197
P71117_CLOBO **[Clostridium**
botulinum] AA
align

Score = 74.3 bits (181), Expect = 5e-12
 Identities = 66/288 (22%), Positives = 127/288 (43%), Gaps = 41/288 (14%)

Query: 16 IYTNDTILIEMFNKNYNSXXXXXXXXXRYKDNNLI--DLSGYGAKVEVYDGVELNDKNQF 73
 + T++T LI K E . +DNN + D+SG V+ D + L
 Sbjct: 819 LITSETDLI---KEEKESDYNLFLFTLQEDNNKVIEDISGKNTLVKYSDSISLTVYGNG 874

Query: 74 KLTSSANSKIRVTQNQNIIFNSVFLLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNN 133
 V+ * N + FS+ FW+R N G ++ I ++ +I +N
 Sbjct: 875 DALYLKEPDESVSFSNKAFENGTLNSFSICFWLR----NLG-EDIITSK--LIENKADN 926

Query: 134 SGWKISIRGNRIIWTLIDINGKTKSFFEYNIREDISEYINR-WFFVTITNNL--NNAKI 190
 GW+I N ++++++D NG +++++ +S+ T+ W+++++ + + N I
 Sbjct: 927 CGWEIYFENNGLVFSIVDCNGNEENIY-----LSDVISKNWYYISISIDRLRNQLLI 978

Query: 191 YINGKLESNTDIKDIRREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIIEERYK 250
 +IN KL +N I+ I + ++ I + + I++ ST N ++ + Y
 Sbjct: 979 FINDKLIAQSIEQILNIYSSNTISL----VNENNPIYIEGLSILNRSITSEEVNNYF 1033

Query: 251 IQSYSEYLKDWFGNPLMYNKEYYMFN-----AGNKNSYIKLK 287
 + Y++D G L YNK Y ++N N N Y+ +K
 Sbjct: 1034 SYLNNSYIRDISGERLEYNKTYELYNYVFPENSLYEVTENNIYLSIK 1081

tr O87710 **NTNH protein [ntnh] [Clostridium baratii]** 1160 AA
O87710_9CLOT align

Score = 74.3 bits (181), Expect = 5e-12
 Identities = 87/357 (24%), Positives = 157/357 (43%), Gaps = 50/357 (14%)

Query: 6 LKTIMPFDSLTIYTNDTILIE----MFNKYN-----SEXXXXXXXRYKDNNLI-DLS 53
 L+ IM L+ D + IE +FN Y S + +D N+I D S
 Sbjct: 759 LQLIMQNSLNSLNFDL DIEKIKCLFSYTRLLIKQSSPYELSLYAFOGEDKNVIGDGS 818

Query: 54 GYGAKEVYDGVEL--NDKNQFKLTSSANSKIRVTQN--QNIIFNSVFLLDFSVSFWIRIP 109
 G VE + + L N + +N + T + +N + NS FS+ FW+R
 Sbjct: 819 GKNTLVEYTNDIGLIYGINNNALYLNQSNQSVFTNDYFENGLTNS---FSIYFWLR-- 872

Query: 110 KYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSFFEYNIREDI 169
 D I++ +I+ +N GW+I + N +++ +ID NG K ++ I
 Sbjct: 873 NLGKDIIKS-----KLSSKLDNCWEIYLEDNGLVFNIIDSNGSYKKIY-----I 918

Query: 170 SEYINRWFVTITNN--LNNAKIYINGKLESNTDIKDIREVIANGEIIIFKLDGDIDRTQF 227
 S+ N W ++ I + * I++N L + N DIKDI + ++ I *
 Sbjct: 919 SDMNNSWNYIAISVDRLKEQLLIFVNDVLVANEDIKDLNLISSNTISL----VSENNQ 973

Query: 228 IWMKYFSIFNTELSQSNIEERYKIQSSEYLKDFWGNPLMYNKEYYMFN-AGNKNSYIKL 286
 I ++ SI NT +++ + Y + Y+++ L YNK+Y +FN +K K+
 Sbjct: 974 ICIEGLSILNTNITKEEVNNYFADLNNSYIRNGNEERLEYNKKYNNLFNYVFSKTPICKV 1033

Query: 287 KKDSPVGEILTRSKYNQNSKYINYRDLYI--GEKFIIRRKSNSQSINDDIVRKEDYI 341
 ++ + + + N N K +++ L + +K++ + SI DD KE ?+
 Sbjct: 1034 NHNNKI-YLSINNDDNLNVKPLSFMLLSVDSNKKYVQKCDEVIISILDD---KERYL 1086

tr 069277 Nontoxic-nonhaemagglutinin [ntnh] [Clostridium 1198
069277_CLOBO botulinum] AA
align

Score = 74.3 bits (181), Expect = 5e-12
 Identities = 54/219 (24%), Positives = 102/219 (45%), Gaps = 39/219 (17%)

Query: 88 NQNIIFNSVFLD-----FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSWKISIR 141
 NQ+I F++ F + FS+ FW+R D I++ +I ++N GW+I +
 Sbjct: 884 NQSISFSNDFFENGLTNSFSIYFWLR--NLGKDTIKS----KLIGSKEDNCGWEIYFQ 935

Query: 142 GNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFVTITNNLNNAK--IYINGKLESN 199
 +++ +ID NG K+++ D+S N W ++TI+ + + I+I+ L +N
 Sbjct: 936 DTGLVFNMIDSNGNEKNIYLS----DVSN--NSWHYITISVDRLKEQLLIFIDDNLVAN 988

Query: 200 TDIKDIREVIANGEIIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSSEYLK 259
 TK+I + ++ I + ++ I+++ ST N ++ + Y + Y++
 Sbjct: 989 ESIKEILNIYSSNTISL----VNENNPIYVEGLSILNRSITSEEVNNYFTYLNNSYIR 1043

Query: 260 DFWGNPLMYNKEYYMFN-----AGNKNSYIKLK 287
 D G L YNK Y ++N N N Y+ +K
 Sbjct: 1044 DISGERLEYNKTYELYNYVFPESSLYEVTENNNIYLSIK 1082

tr 033871 Nontoxic-nonhemagglutinin component [ntnh/B] 1197
033871_CLOBO [Clostridium botulinum] AA
align

Score = 74.3 bits (181), Expect = 5e-12
 Identities = 66/288 (22%), Positives = 127/288 (43%), Gaps = 41/288 (14%)

Query: 16 IYTNDTILIEMFNKNSEXXXXXXXXXRYKDNNLI--DLSGYGAKVEVYDGVELNDKNQF 73
 + T++T LI K E +UNN + D+SG V+ D + L
 Sbjct: 819 LITSETDLI----KEEKESDYNLFLFTLQEDNNKVIEDISGKNTLVKYSDSISLVYGVNG 874

Query: 74 KLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNN 133
 V+ + N + FS+ FW+R N G ++ I ++ +I +N
 Sbjct: 875 DALYLKEPDESFSNKAFENGTLNSFSICFWLR----NLG-EDIITSK--LIENKADN 926

Query: 134 SGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINR-WFFVTITNNL--NNAKI 190
 GN+I N ++++D NG +++++ +S+ I++ W+++I+ + N I

Query: 170 SEYINRWFFVTITNN--LNNAKIYINGKLESNTDIKDIREVIANGEIIIFKLDGDIDRTQF 227
 S+ N W ++ I+ + I++N L +N DIKDI + ++ I +
 Sbjct: 919 SDMNNSWNYIAISVDRLKEQLLIFVNDVLVANEDIKDILNIYSSNTISL----VSENNQ 973

Query: 228 IWMKYFSIFNTELSQSNIEERYKIQSSEYLKDFWGNPLMYNKEYYMFN-AGNKNSYIKL 286
 I ++ ST NT +++ + Y + Y+++ L YNK+Y +FN +K K+
 Sbjct: 974 ICIEGLSILNTNITKEEVLNNSYADLNNSYIRNGNEERLEYNKKYLNLYVFSKTPICKV 1033

Query: 287 KKDSPVGEILTRSKYNQNSKYINYRDLYI--GEKFIIRRKSNSQSINDIVRKEDYI 341
 ++ + + + N N K +++ L + +K++ + SI DD KE ??
 Sbjct: 1034 NHNNKI-YLSINNDDNLNVKPLSFMLLSVDSNKKYVQKCDEVIISILDD---KERYL 1086

tr O69277 Nontoxic-nonhaemagglutinin [ntnh] [Clostridium 1198
O69277_CLOBO botulinum] AA
align

Score = 74.3 bits (181), Expect = 5e-12
 Identities = 54/219 (24%), Positives = 102/219 (45%), Gaps = 39/219 (17%)

Query: 88 NQNIIFNSVFLD-----FSVFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIR 141
 NQ+I F++ F + FS+ FW+R D I++ +I ++N GW+I +
 Sbjct: 884 NQSIISFSNDFFENGLTNSFSIYFWLR--NLGKDTIKS-----KLIGSKEDNCGWEIYFQ 935

Query: 142 GNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNNLNNAK--IYINGKLESN 199
 +++ +ID NG K+++ D+S N W ++T+ + + I+I+ L +N
 Sbjct: 936 DTGLVFNMIDSNGNEKNIYLS----DVSN--NSWHYITISVDRLKEQLLIFIDDNLVAN 988

Query: 200 TDIKDIREVIANGEIIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSSEYLK 259
 IK+I + ++ I + ++ I+++ ST N ++ + Y + Y++
 Sbjct: 989 ESIKEILNIYSSNTISL----VNENNPIYVEGLSILNRSITSEEVVNNYFTYLNNSYIR 1043

Query: 260 DFWGNPLMYNKEYYMFN-----AGNKNSYIKLK 287
 D G L YNK Y ++N N N Y+ +K
 Sbjct: 1044 DISGERLEYNKTYELYNYVFPESSLYEVTENNNIYLSIK 1082

tr O33871 Nontoxic-nonhemagglutinin component [ntnh/B] 1197
O33871_CLOBO [Clostridium botulinum] AA
align

Score = 74.3 bits (181), Expect = 5e-12
 Identities = 66/288 (22%), Positives = 127/288 (43%), Gaps = 41/288 (14%)

Query: 16 IYTNDTILIEMFNKYNSEXXXXXXXXXRYKDNLLI--DL SGYGA KV E VYDG VELNDKNQF 73
 + T++T LT X S +DNN + D+SG V+ D + L
 Sbjct: 819 LITSETDLI----KEEKESDYNLFIFTLQEDNNKVIEDISGKNTLVKYSDSISLVYGVNG 874

Query: 74 KLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNN 133
 V+ + N + FS+ FW+R N G ++ I ++ +I +N
 Sbjct: 875 DALYLKEPDESVSFSNKAFENGTLNSFSICFWLR----NLG-EDIITSK--LIENKADN 926

Query: 134 SGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINR-WFFVTITNNL--NNAKI 190
 GW+I N + + + +D NG + + + + +S+ I++ W++ + + + + N I

Sbjct: 927 CGWEIYFENNGLVFSIVDCNGNEENIY-----LSDVISKWNYYISISIDRLRNQLLI 978
 Query: 191 YINGKLESNTDIKDIREVIANGEIIIFKLDGIDRTQFIWMKYFSIFNTELSQSNIERYK 250
 +IN KL +N I+ I + ++ I ++ I+++ SI N ++ + Y
 Sbjct: 979 FINDKLIANQSIEQILNIYSSNTISL----VNENNPIYIEGLSILNRSITSEEVNNYF 1033
 Query: 251 IQSYSEYLKDFWGNPLMYNKEYYMFN-----AGNKNSYIKLK 287
 + Y++D G L YNK Y ++N N N Y+ +K
 Sbjct: 1034 SYLNNSYIRDISGERLEYNKTYELYNYVFPENSLEYVTENNNIYLSIK 1081

tr Q45893 **NTNH protein [ntnh] [Clostridium botulinum]** 1198 AA
Q45893_CLOBO align
 Score = 73.9 bits (180), Expect = 7e-12
 Identities = 54/219 (24%), Positives = 102/219 (45%), Gaps = 39/219 (17%)
 Query: 88 NQNIIFNSVFLD-----FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIR 141
 NQ+T F++ F + FS+ FW+R D T++ +I ++N GW+I +
 Sbjct: 884 NQSISFSNDFFENGLTNSFSIYFWLR--NLGKDTIKS-----KLIGSKEDNCGWEIYFQ 935
 Query: 142 GNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNNLNNAK--IYINGKLESN 199
 +++ +ED NG K+++ D+S N W ++T+ + + + T+T+ L +N
 Sbjct: 936 DTGLVFNMIDSNGNEKNIYLS----DVSN--NSWHYITISVDRLKEQLLIFIDDNLVAN 988
 Query: 200 TDIKDIREVIANGEIIIFKLDGIDRTQFIWMKYFSIFNTELSQSNIERYKIQSYSEYLK 259
 IK+I + ++ I ++ I+++ SI N ++ + Y + Y++
 Sbjct: 989 GSIKEILNIYSSNTISL----VNENNPIYVEGLSILNRSITSEEVNNYFTYLNNSYIR 1043
 Query: 260 DFWGNPLMYNKEYYMFN-----AGNKNSYIKLK 287
 D G L YNK Y ++N N N Y+ +K
 Sbjct: 1044 DISGERLEYNKTYELYNYVFPESSLYEVTEENNNIYLSIK 1082

tr Q9LBR2 **NTNHA [ntnha] [Clostridium botulinum]** 1196 AA
Q9LBR2_CLOBO align
 Score = 73.6 bits (179), Expect = 9e-12
 Identities = 61/261 (23%), Positives = 115/261 (43%), Gaps = 38/261 (14%)
 Query: 43 RYKDNNLI-DLSGYGAKVEVYDGVEL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLD 99
 R ++N+I D+SG ++ + VEL + S N + + N N + +
 Sbjct: 843 RGPNSNIIEDISGKNTLIQYTESVELVYGVNGESLYLKSPNETVEFSNN--FFTNGLTNN 900
 Query: 100 FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSV 159
 F++ FW+R K+D I N+ NN GW+I N +++ +ID NG +SV
 Sbjct: 901 FTICFWLRFTG-KDDDKTRLIGNKV-----NNCGWEIYFEDNGLVFEIIDSNGNQESV 952
 Query: 160 FFEYNIREDISEYINRWFFVTITNN--LNNAKIYINGKLESNTDIKDIREVIANGEIIIFK 217
 + I N W++ +I+ + + I+IN K +N I+ I + + I
 Sbjct: 953 YLSNVIN-----NNWYYISISVDRLKDQLLIFINDKVNANVSIEQILNIYSTNVISL- 1004
 Query: 218 LDGGDIDRTQFIWMKYFSIFNTELSQSNIERYKIQSYSEYLKDFWGNPLMYNKEYYMFN- 276
 +++ I+++ S+ + ++ + Y + Y++D + L YNK Y ++N
 Sbjct: 1005 ----VNKNNSIYVEELSVLDKPVASEEVIRNYFSYLDNSYIRDSSKSLEYNKNYQLNY 1060

Subjct: 927 CGWEIYFENNGLVFSIVDCNGNEENIY-----LSDVISKNWYYISISIDRLRNQLLI 978
 Query: 191 YINGKLESNTDIKDIREVIANGEIIIFKLDGIDRTQFIWMKYFSIFNTELSQSNIERYK 250
 +IN KL +N I+ T + ++ I +++ I+++ SI N ++ + Y
 Subjct: 979 FINDKLIANQSIEQILNIYSSNTISL----VNENNPIYIEGLSILNRSITSEEVNNYF 1033
 Query: 251 IQSYSEYLKDFWGNPLMYNKEYMFN-----AGNKNSYIKLK 287
 + Y++D G L YNK Y ++N N N Y+ +K
 Subjct: 1034 SYLNNNSYIRDISGERLEYNKTYELYNYVFPENSLYEVTEENNNIYLSIK 1081

tr Q45893 NTN_H protein [ntnh] [Clostridium botulinum] 1198 AA align
Q45893_CLOBO

Score = 73.9 bits (180), Expect = 7e-12
 Identities = 54/219 (24%), Positives = 102/219 (45%), Gaps = 39/219 (17%)

Query: 88 NQNIIIFNSVF~~L~~-----FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIR 141
 NQ+I F++ F + FS+ FW+R D T++ +I ++N CW+I +
 Subjct: 884 NQSISFSNDFFENG~~L~~TNSFSIYFWLR--NLGKDTIKS-----KLIGSKEDNC~~G~~WEIYFQ 935

Query: 142 GNRIIWT~~L~~IDINGKTKSVFFEYNIREDISEY~~I~~NRWFFVTITNNLNNAK--IYINGKLESN 199
 +++ +ID NG K++ D+S N W ++T+ + + I+I+ L +N
 Subjct: 936 DTGLVFNMIDSNGNEKNIYLS----DVSN--NSWHYITISVDRLKEQLLIFIDDNLVAN 988

Query: 200 TD~~I~~KDIREVIANGEIIIFKLDGIDRTQFIWMKYFSIFNTELSQSNIERYKIQSYSEYLK 259
 IK+I + ++ I +++ I+++ SI N ++ + Y + Y++
 Subjct: 989 GS~~I~~KEILNIYSSNTISL----VNENNPIYVEGLSILNRSITSEEVNNYFTYLNNSYIR 1043

Query: 260 DFWGNPLMYNKEYMFN-----AGNKNSYIKLK 287
 D G L YNK Y ++N N N Y+ +K
 Subjct: 1044 DISGERLEYNKTYELYNYVFPESSLYEVTEENNNIYLSIK 1082

tr Q9LBR2 NTN_HA [ntnha] [Clostridium botulinum] 1196 AA align
Q9LBR2_CLOBO

Score = 73.6 bits (179), Expect = 9e-12
 Identities = 61/261 (23%), Positives = 115/261 (43%), Gaps = 38/261 (14%)

Query: 43 RYKDNNLI-DLSGYGAKVEVYDGVEL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVF~~L~~ 99
 R ++N+I D+SG ++ + VEL + S N + . + N N + +
 Subjct: 843 RGPN~~S~~NIIEDISGKNTLIQYTESVELVYGVNGESLYLKSPNETVEFSNN--FFTNGLTNN 900

Query: 100 FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKS~~V~~ 159
 F++ FW+R K+D I N+ NN CW+I N + + + ID NG +SV
 Subjct: 901 FTICFWLRFTG-KDDDKTRLIGNKV-----NNCGWEIYFEDNGLVFEIIDSNGNQESV 952

Query: 160 FFEYNIREDISEY~~I~~NRWFFVTITNN--LNNAKIYINGKLESNTDIKDIREVIANGEIIIFK 217
 + I N W + + + I + + + I+IN K +N I+ I + + I
 Subjct: 953 YLSNVIN-----NNWYYISISVDRLKDQLLIFINDKVNANVSIEQILNIYSTNVISL- 1004

Query: 218 LDGDIDRTQFIWMKYFSIFNTELSQSNIERYKIQSYSEYLKDFWGNPLMYNKEYMFN- 276
 + + + I + + + S + + + + Y + Y++D + L YNK Y ++N
 Subjct: 1005 ---VNKNNSIYVEELSVLDKPVASEEVIRNYFSYLDNSYIRDSSKSLEYNKNYQLNY 1060

Query: 277 -----AGNKNSYIKLK 287
 N SY+ LK
 Sbjct: 1061 VFPETSLYEVNDNNNKSYLSLK 1081

sp P46081 Botulinum neurotoxin type C1, nontoxic component 1196
 BXCN_CLOBO [Clostridium AA
 botulinum] align

Score = 72.0 bits (175), Expect = 3e-11
 Identities = 60/256 (23%), Positives = 111/256 (42%), Gaps = 37/256 (14%)

Query: 47 NNLIDLSGYGAKVEVYDGVEL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSF 104
 N + D+SG ++ + +EL + S N I+ + N + +F++ F
 Sbjct: 848 NIIEDISGKNTLIQYTESIELVYGVNGESLYLKSPNETIKFSNK--FFTNGLTNNFTICF 905

Query: 105 WIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLDINGKTKSVFFEYN 164
 W+R KND I N+ NN GW+I N +++ +ID NG +SV+ N
 Sbjct: 906 WLRFTG-KNDDKTRLIGNKV-----NNCGWEIYFEDNGLVFEIIDSNGNQESVYLS-N 956

Query: 165 IREDISEYINRWFFVTITNN--LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDI 222
 I D W+++I+ + + I+IN K +N I I + + I +
 Sbjct: 957 IIND-----NWYYISISVDRLKQDQLLIFINDKNVANVSIDQILSIYSTNIISL----V 1005

Query: 223 DRTQFIWMKYFSIFNTELSQSNIIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFN----- 276
 ++ T+++ S+ + ++ + Y + Y++D + L YNK Y ++N
 Sbjct: 1006 NKNNSIYVEELSVLDNPITSEEVIRNYFSYLDNSYIRDSSKSLLEYNKNYQLYNYVF PET 1065

Query: 277 -----AGNKNSYIKLK 287
 N SY+ LK
 Sbjct: 1066 SLYEVNDNNNKSYLSLK 1081

tr Q93HT4 NTNHA [ntnha] [Clostridium botulinum] 1196 AA
Q93HT4_CLOBO align

Score = 72.0 bits (175), Expect = 3e-11
 Identities = 60/256 (23%), Positives = 111/256 (42%), Gaps = 37/256 (14%)

Query: 47 NNLIDLSGYGAKVEVYDGVEL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSF 104
 N + D+SG ++ + +EL + S N I+ + N + +F++ F
 Sbjct: 848 NIIEDISGKNTLIQYTESIELVYGVNGESLYLKSPNETIKFSNK--FFTNGLTNNFTICF 905

Query: 105 WIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLDINGKTKSVFFEYN 164
 W+R KND I N+ NN GW+I N +++ +ID NG +SV+ N
 Sbjct: 906 WLRFTG-KNDDKTRLIGNKV-----NNCGWEIYFEDNGLVFEIIDSNGNQESVYLS-N 956

Query: 165 IREDISEYINRWFFVTITNN--LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDI 222
 I D W+++I+ + + I+IN K +N I I + + I +
 Sbjct: 957 IIND-----NWYYISISVDRLKQDQLLIFINDKNVANVSIDQILSIYSTNIISL----V 1005

Query: 223 DRTQFIWMKYFSIFNTELSQSNIIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFN----- 276
 ++ T+++ S+ + ++ + Y + Y++D + L YNK Y ++N
 Sbjct: 1006 NKNNSIYVEELSVLDNPITSEEVIRNYFSYLDNSYIRDSSKSLLEYNKNYQLYNYVF PET 1065

Query: 277 -----AGNKNSYIKLK 287
 N SY+ LK
 Sbjct: 1061 VFPETSLYEVNDNNKSYLSLK 1081

sp P46081 Botulinum neurotoxin type C1, nontoxic component 1196
 BXCN_CLOBO [Clostridium AA
 botulinum] align

Score = 72.0 bits (175), Expect = 3e-11
 Identities = 60/256 (23%), Positives = 111/256 (42%), Gaps = 37/256 (14%)

Query: 47 NNLIDLSGYGAKVEVYDGVEL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSF 104
 N + D+SG ++ + +EL + S N I+ + N + +F++ F
 Sbjct: 848 NIIEDISGKNTLIQYTESIELVYGVNGESLYLKSPNETIKFSNK--FFTNGLTNNFTICF 905

Query: 105 WIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLDINGKTKSVFFEYN 164
 W+R KND I N+ MN GW+I N +++ +ID NG +SV+ N
 Sbjct: 906 WLRFTG-KNDDKTRLIGNKV-----NNCGWEIYFEDNGLVFEIIDSNGNQESVYLS-N 956

Query: 165 IREDISEYINRWFFVTITNN--LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDI 222
 I D W+***I+ + + I+IN K +N I I + + I +
 Sbjct: 957 IIND-----NWYYISISVDRLKQDQLLIFINDKVNANVSIDQILSIYSTNIISL----V 1005

Query: 223 DRTQFIWMKYFSIFNTELSQSNIIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFN----- 276
 ++ T+++ S+ + ++ + Y + Y++D + L YNK Y ++N
 Sbjct: 1006 NKNNNSIYVEELSVLDNPITSEEVIRNYFSYLDNSYIRDSSKSLLEYNKNYQLYNYVFPET 1065

Query: 277 -----AGNKNSYIKLK 287
 N SY+ LK
 Sbjct: 1066 SLYEVNDNNKSYLSLK 1081

tr Q93HT4 NTNHA [ntnha] [Clostridium botulinum] 1196 AA
Q93HT4_CLOBO align

Score = 72.0 bits (175), Expect = 3e-11
 Identities = 60/256 (23%), Positives = 111/256 (42%), Gaps = 37/256 (14%)

Query: 47 NNLIDLSGYGAKVEVYDGVEL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSF 104
 N + D+SG ++ + +EL + S N I+ + N + +F++ F
 Sbjct: 848 NIIEDISGKNTLIQYTESIELVYGVNGESLYLKSPNETIKFSNK--FFTNGLTNNFTICF 905

Query: 105 WIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLDINGKTKSVFFEYN 164
 W+R KND I N+ MN GW+I N +++ +ID NG +SV+ N
 Sbjct: 906 WLRFTG-KNDDKTRLIGNKV-----NNCGWEIYFEDNGLVFEIIDSNGNQESVYLS-N 956

Query: 165 IREDISEYINRWFFVTITNN--LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDI 222
 I D W+***I+ + + I+IN K +N I I + + I +
 Sbjct: 957 IIND-----NWYYISISVDRLKQDQLLIFINDKVNANVSIDQILSIYSTNIISL----V 1005

Query: 223 DRTQFIWMKYFSIFNTELSQSNIIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFN----- 276
 ++ T+++ S+ + ++ + Y + Y++D + L YNK Y ++N
 Sbjct: 1006 NKNNNSIYVEELSVLDNPITSEEVIRNYFSYLDNSYIRDSSKSLLEYNKNYQLYNYVFPET 1065

Query: 277 -----AGNKNSYIKLK 287
 N SY+ LK
 Sbjct: 1066 SLYEVNDNNKSYLSLK 1081

tr Q45916 138kDa protein associated with BoNT /C1-haemagglutinin 1196
 Q45916_CLOBO complex AA
 [CHn-138] [Clostridium botulinum] align

Score = 72.0 bits (175), Expect = 3e-11
 Identities = 60/256 (23%), Positives = 111/256 (42%), Gaps = 37/256 (14%)

Query: 47 NNLIDLSGYGAKVEVYDGVEL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSF 104
 N + D+SG ++ + +EL + S N I+ + N + +F++ F
 Sbjct: 848 NIIEDISGKNTLIQYTESIELVYGVNGESLYLKSPNETIKFSNK--FFTNGLTNNFTICF 905

Query: 105 WIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLDINGKTKSFFEYN 164
 W+R KND I N+ NN GW+I N +++ +ID NG +SV+ N
 Sbjct: 906 WLRFTG-KNDDKTRLIGNKV-----NNCGWEIYFEDNGLVFEIIDSNGNQESVYLS-N 956

Query: 165 IREDISEYINRWFFVTITNN--LNNAKIYINGKLESNTDIKDIREVIANGEIFKLDGDI 222
 I D W+++I+ + + I+IN K +N I I + + I +
 Sbjct: 957 IIND-----NWYYISISVDRLKQDQLLIFINDKNVANVSIDQILSIYSTNIISL----V 1005

Query: 223 DRTQFIWMKYFSIFNTELSQSNIIEERYKIQSSEYLKDFWGNPLMYNKEYYMFN----- 276
 ++ T+++ S+ + ++ + Y + Y++D + L YNK Y ++N
 Sbjct: 1006 NKNNSIYVEELSVDNPITSEEVIRNYFSYLDNSYIRDSSKSLLEYNKNYQLYNYVFPET 1065

Query: 277 -----AGNKNSYIKLK 287
 N SY+ LK
 Sbjct: 1066 SLYEVNDNNKSYLSLK 1081

tr Q9ZX77 NTNH [ntnh] [Clostridium botulinum D 1196 AA
 Q9ZX77_CBDP bacteriophage] align

Score = 72.0 bits (175), Expect = 3e-11
 Identities = 60/256 (23%), Positives = 111/256 (42%), Gaps = 37/256 (14%)

Query: 47 NNLIDLSGYGAKVEVYDGVEL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSF 104
 N + D+SG ++ + +EL + S N I+ + N + +F++ F
 Sbjct: 848 NIIEDISGKNTLIQYTESIELVYGVNGESLYLKSPNETIKFSNK--FFTNGLTNNFTICF 905

Query: 105 WIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLDINGKTKSFFEYN 164
 W+R KND I N+ NN GW+I N +++ +ID NG +SV+ N
 Sbjct: 906 WLRFTG-KNDDKTRLIGNKV-----NNCGWEIYFEDNGLVFEIIDSNGNQESVYLS-N 956

Query: 165 IREDISEYINRWFFVTITNN--LNNAKIYINGKLESNTDIKDIREVIANGEIFKLDGDI 222
 I D W+++I+ + + I+IN K +N I I + + I +
 Sbjct: 957 IIND-----NWYYISISVDRLKQDQLLIFINDKNVANVSIDQILSIYSTNIISL----V 1005

Query: 223 DRTQFIWMKYFSIFNTELSQSNIIEERYKIQSSEYLKDFWGNPLMYNKEYYMFN----- 276
 ++ T+++ S+ + ++ + Y + Y++D + L YNK Y ++N
 Sbjct: 1006 NKNNSIYVEELSVDNPITSEEVIRNYFSYLDNSYIRDSSKSLLEYNKNYQLYNYVFPET 1065

Query: 277 -----AGNKNSYIKLK 287
 N SY+ LK
 Sbjct: 1066 SLYEVNDNNKSYLSLK 1081

tr Q45916 138kDa protein associated with BoNT /C1-haemagglutinin 1196
Q45916_CLOBO complex AA
[CHn-138] [Clostridium botulinum] align

Score = 72.0 bits (175), Expect = 3e-11
 Identities = 60/256 (23%), Positives = 111/256 (42%), Gaps = 37/256 (14%)

Query: 47 NNLIDLSGYGAKVEVYDGVEL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSF 104
 N + D+SG ++ + +EL + S N I+ + N + +F++ F
 Sbjct: 848 NIIEDISGKNTLIQYTESIELVYGVNGESLYLKSPNETIKFSNK--FFTNGLTNNFTICF 905

Query: 105 WIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLDINGKTKSVFFEYN 164
 W+R KND I N+ NN GW+I N +++ +ID NG +SV+ N
 Sbjct: 906 WLRFTG-KNDDKTRLIGNKV-----NNCGWEIYFEDNGLVFEIIDSNGNQESVYLS-N 956

Query: 165 IREDISEYINRWFFVTITNN--LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDI 222
 I D W+++I+ + + I+IN K +N I I + + I +
 Sbjct: 957 IIND-----NWYYISISVDRLKQDQLLIFINDKVNANVSIDQILSIYSTNIISL----V 1005

Query: 223 DRTQFIWMKYFSIFNTELSQSNEERYKIQSYSEYLKDFWGNPLMYNKEYYMFN----- 276
 ++ I+++ S+ + ++ + Y + Y++D + L YNK Y ++N
 Sbjct: 1006 NKNNSIYVEELSVDNPITSEEVIRNYFSYLDNSYIRDSSKSLLEYNKNYQLYNYVF PET 1065

Query: 277 -----AGNKNSYIKLK 287
 N SY+ LK
 Sbjct: 1066 SLYEVNDNNKSYLSLK 1081

tr Q9ZX77 NTN_H [ntnh] [Clostridium botulinum D 1196 AA
Q9ZX77_CBDP bacteriophage] align

Score = 72.0 bits (175), Expect = 3e-11
 Identities = 60/256 (23%), Positives = 111/256 (42%), Gaps = 37/256 (14%)

Query: 47 NNLIDLSGYGAKVEVYDGVEL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSF 104
 N + D+SG ++ + +EL + S N I+ + N + +F++ F
 Sbjct: 848 NIIEDISGKNTLIQYTESIELVYGVNGESLYLKSPNETIKFSNK--FFTNGLTNNFTICF 905

Query: 105 WIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLDINGKTKSVFFEYN 164
 W+R KND I N+ NN GW+I N +++ +ID NG +SV+ N
 Sbjct: 906 WLRFTG-KNDDKTRLIGNKV-----NNCGWEIYFEDNGLVFEIIDSNGNQESVYLS-N 956

Query: 165 IREDISEYINRWFFVTITNN--LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDI 222
 I D W+++I+ + + I+IN K +N I I + + I +
 Sbjct: 957 IIND-----NWYYISISVDRLKQDQLLIFINDKVNANVSIDQILSIYSTNIISL----V 1005

Query: 223 DRTQFIWMKYFSIFNTELSQSNEERYKIQSYSEYLKDFWGNPLMYNKEYYMFN----- 276
 ++ I+++ S+ + ++ + Y + Y++D + L YNK Y ++N
 Sbjct: 1006 NKNNSIYVEELSVDNPITSEEVIRNYFSYLDNSYIRDSSKSLLEYNKNYQLYNYVF PET 1065

Query: 277 -----AGNKNSYIKLK 287
 N SY+ LK
 Sbjct: 1066 SLYEVNDNNKSYLSLK 1081

tr Q38197 ANTP-139 protein [ANTP-139] [Clostridium botulinum] 1196
Q38197_9VIRU phage 1C] AA align

Score = 72.0 bits (175), Expect = 3e-11
 Identities = 60/256 (23%), Positives = 111/256 (42%), Gaps = 37/256 (14%)

Query: 47 NNLIDLSGYGAKVEVYDGVEL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSF 104
 N + D+SG ++ + +EL + S N I+ + N + +F++ F
 Sbjct: 848 NIIEDISGKNTLIQYTESIELVYGVNGESLYLKSPNETIKFSNK--FFTNGLTNNFTICF 905

Query: 105 WIRIPKYKNDGIQNYIHNNEYTIINCMKNNSGWKISIRGNRIWTLIDINGKTKSVFFEYN 164
 W+R KND I N+ NN GW+I N +++ +ID NG +SV+ N
 Sbjct: 906 WLRFTG-KNDDKTRLIGNKV-----NNCGWEIYFEDNGLVFEIIDSNGNQESVYLS-N 956

Query: 165 IREDISEYINRWFFVTITNN--LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDI 222
 I D W+++I+ + + I+IN K +N I I + + I +
 Sbjct: 957 IIND-----NWYYISISVDRLKQDQLLIFINDKVNANVSIDQILSIYSTNIISL----V 1005

Query: 223 DRTQFIWMKYFSIFNTELSQSNEERYKIQSYSEYLKDFWGNPLMYNKEYYMFN----- 276
 ++ I+++ S+ + ++ + Y + Y++D + L YNK Y ++N
 Sbjct: 1006 NKNNSIYVEELSVLDNPITSEEVIRNYFSYLDNSYIRDSSKSLLEYNKNYQLYNYVFPET 1065

Query: 277 -----AGNKNSYIKLK 287
 N SY+ LK
 Sbjct: 1066 SLYEVNDNNKSYLSLK 1081

tr Q53550 Progenitor toxin L nontoxic-nonhemagglutinin component 1196
Q53550_CLOBO [Clostridium botulinum] AA align

Score = 71.6 bits (174), Expect = 3e-11
 Identities = 60/256 (23%), Positives = 111/256 (42%), Gaps = 37/256 (14%)

Query: 47 NNLIDLSGYGAKVEVYDGVEL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSF 104
 N + D+SG ++ + +EL + S N I+ + N + +F++ F
 Sbjct: 848 NIIEDISGKNTFIQYTESIELVYGVNGESLYLKSPNETIKFSNK--FFTNGLTNNFTICF 905

Query: 105 WIRIPKYKNDGIQNYIHNNEYTIINCMKNNSGWKISIRGNRIWTLIDINGKTKSVFFEYN 164
 W+R KND I N+ NN GW+I N +++ +ID NG +SV+ N
 Sbjct: 906 WLRFTG-KNDDKTRLIGNKV-----NNCGWEIYFEDNGLVFEIIDSNGNQESVYLS-N 956

Query: 165 IREDISEYINRWFFVTITNN--LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDI 222
 I D W++++I+ + + I+IN K +N I I + + I +
 Sbjct: 957 IIND-----NWYYISISVDRLKQDQLLIFINDKVNANVSIDQILSIYSTNIISL----V 1005

Query: 223 DRTQFIWMKYFSIFNTELSQSNEERYKIQSYSEYLKDFWGNPLMYNKEYYMFN----- 276
 ++ I+++ S+ + ++ + Y + Y++D + L YNK Y ++N

Query: 277 -----AGNKNSYIKLK 287
 N SY+ LK
 Sbjct: 1066 SLYEVNDNNKSYLSLK 1081

tr Q38197 ANTP-139 protein [ANTP-139] [Clostridium botulinum] 1196
Q38197_9VIRU phage 1C AA align

Score = 72.0 bits (175), Expect = 3e-11
 Identities = 60/256 (23%), Positives = 111/256 (42%), Gaps = 37/256 (14%)

Query: 47 NNLIDLSGYGAKVEVYDGVEL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSF 104
 N + D+SG + + + +EL + S N I+ + N + +F++ F
 Sbjct: 848 NIIEDISGKNTLIQYTESIELVYGVNGESLYLKSPNETIKFSNK--FFTNGLTNNFTICF 905

Query: 105 WIRIPKYKNDGIQNYIHNNEYTIINCMKNNSGWKISIRGNRIWTLIDINGKTKSVFFEYN 164
 W+R KND I N+ NN GW+I N +++ +ID NG +SV+ N
 Sbjct: 906 WLRFTG-KNDDKTRLIGNKV-----NNCGWEIYFEDNGLVFEIIDSNGNQESVYLS-N 956

Query: 165 IREDISEYINRWFFVTITNN--LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDI 222
 I D W+++ +I+ + + T+IN K +N I I + + I +
 Sbjct: 957 IIND-----NWYYISISVDRLKQDQLLIFINDKVNANVSIDQILSIYSTNIISL----V 1005

Query: 223 DRTQFIWMKYFSIFNTELSQSNIIEERYKIQSSEYLKDFWGNPLMYNKEYYMFN----- 276
 ++ T+++ S+ + ++ + Y + Y++D + L YNK Y ++N
 Sbjct: 1006 NKNNSIYVEELSVLDNPITSEEVIRNYFSYLDNSYIRDSSKSLLNEYNKNYQLYNYVFPET 1065

Query: 277 -----AGNKNSYIKLK 287
 N SY+ LK
 Sbjct: 1066 SLYEVNDNNKSYLSLK 1081

tr Q53550 Progenitor toxin L nontoxic-nonhemagglutinin component 1196
Q53550_CLOBO [Clostridium AA align
 botulinum]

Score = 71.6 bits (174), Expect = 3e-11
 Identities = 60/256 (23%), Positives = 111/256 (42%), Gaps = 37/256 (14%)

Query: 47 NNLIDLSGYGAKVEVYDGVEL--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSF 104
 N + D+SG + + + +EL + S N I+ + N + +F++ F
 Sbjct: 848 NIIEDISGKNTFIQYTESIELVYGVNGESLYLKSPNETIKFSNK--FFTNGLTNNFTICF 905

Query: 105 WIRIPKYKNDGIQNYIHNNEYTIINCMKNNSGWKISIRGNRIWTLIDINGKTKSVFFEYN 164
 W+R KND I N+ NN GW+I N +++ +ID NG +SV+ N
 Sbjct: 906 WLRFTG-KNDDKTRLIGNKV-----NNCGWEIYFEDNGLVFEIIDSNGNQESVYLS-N 956

Query: 165 IREDISEYINRWFFVTITNN--LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDI 222
 I D W+++ +I+ + + T+IN K +N I I + + I +
 Sbjct: 957 IIND-----NWYYISISVDRLKQDQLLIFINDKVNANVSIDQILSIYSTNIISL----V 1005

Query: 223 DRTQFIWMKYFSIFNTELSQSNIIEERYKIQSSEYLKDFWGNPLMYNKEYYMFN----- 276
 ++ T+++ S+ + ++ + Y + Y++D + L YNK Y ++N

Sbjct: 1006 NKNNSIYVEELSVLDNPITSEEVIRNYFSYLDNSYIRDSSKSLLEYNKNYQLYNVFPE 1065
Query: 277 -----AGNKNSYIKLK 287
N SY+ LK
Sbjct: 1066 SLYEVNDNNKSYLSLK 1081

tr Q45891 NTNH protein [ntnh] [Clostridium botulinum] 1161 AA
 Q45891_CLOBO align
 Score = 70.9 bits (172), Expect = 6e-11
 Identities = 70/291 (24%), Positives = 127/291 (43%), Gaps = 49/291 (16%)
 Query: 88 NQNIIFNSVFLD-----FSVFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIR 141
 NQ+I F++ F + FS+ FW+R D I++ +I +N GW+T +
 Sbjct: 852 NQSISFSNDFFENGTLNSFSIYFWLR--NLGKDITKS-----KLIGSKEDNCGWEIYFQ 903
 Query: 142 GNRIIWTLIDINGKTGSVFFEYNIREDISEYINRWFFVTITNN--LNNAKIYINGKLESN 199
 +++ +ID NG K+++ D+S N W ++T+ + T+T+ L +N
 Sbjct: 904 DTGLVFNMDNSNGNEKNIYL----SDVSN--NSWHYITISVDRLKEQLLIFIDDNLVAN 956
 Query: 200 TDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSOSNIEERYKIQSYSEYLK 259
 IK+I + ++ I + +D I+++ SI N + + Y + + Y++
 Sbjct: 957 ESIKEILNIYSSNTISL----VDENNPIYVEGLSILNKPTTSQEVLNSYFKVLNNSYIR 1011
 Query: 260 DFWGNPLMYNKEYYMFN-----AGKNNSYIKLKKDSPVGEILTRSK--YNQNS 305
 D L YNK Y ++N M N Y+ + + + +++ K N N
 Sbjct: 1012 DSSEERLEYNKTYQLYNYVFSENPIYEIKQNNNIYLTINNTNNNLQVSKFKLLSINPNK 1071
 Query: 306 KYINYRDLYI-----GEKFI-IRRKSNSQSINDDIVRKEDYIYLDFFNLM 349
 +Y+ D I EK+I I + Q I++ K+ I D F N
 Sbjct: 1072 QYVQKLDEVIISVLDNMEKYIDISENRLQLIDNKNNAKKMIISNDIFISM 1122

tr	<u>Q45880</u>	NtnhA protein [ntnhA] [Clostridium botulinum]	1193 AA	
	Q45880_CLOBO		<u>align</u>	
Score = 68.9 bits (167), Expect = 2e-10				
Identities = 69/291 (23%), Positives = 127/291 (42%), Gaps = 49/291 (16%)				
Query:	88	NQNIIFNSVFLD-----FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIR	141	
Sbjct:	884	NQ+I F++ F + FS+ FW+R D I++ +I ++N GW+I +	NQSISFSNDFFENGTLNSFSIYFWLR--NLGKDTIKS-----KLIGSKEDNCGWEIYFQ	935
Query:	142	GNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNN--LNNAKIYINGKLESN	199	
Sbjct:	936	+++ +ID NG K+++ D+S N W ++TT+ + I+i+ L +N	DTGLVFNMIDSNGNEKNIYL----SDVSN--NSWHYITISVDRLKEQLLIFIDDNLVAN	988
Query:	200	TDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIIEERYKIQSYSEYLK	259	
Sbjct:	989	IK+i + ++ I + + I+i+ SI N + + Y + Y++	ESIKEILNIYSSNTISL----VNENNPIYVEGLSILNKPTTSQEVLNSYFKVLLNSYIR	1043
Query:	260	DFWGNPLMYNKEYYMFN-----AGKNNSYIKLKKDSPVGEILTRSK--YNQNS	305	
Sbjct:	1044	D I Y NK Y ++N N N Y+ + + + +++ K N N	DSSEERLEYNKTYOLYNYVFSENPIYEIKONNNIYLTIINNTNNLNLOVSKFKLLSINPNK	1103

Sbjct: 1006 NKNNNSIYVEELSVLDNPITSEEVIRNYFSYLDNSYIRDSSKSLLEYNKNYQLYNVFPET 1065
Query: 277 -----AGNKNSYIKLK 287
N SY+ LK
Sbjct: 1066 SLYEVNDNNKSYLSLK 1081

tr Q45891 NTNH protein [ntnh] [Clostridium botulinum] 1161 AA
 Q45891_CLOBO align
 Score = 70.9 bits (172), Expect = 6e-11
 Identities = 70/291 (24%), Positives = 127/291 (43%), Gaps = 49/291 (16%)
 Query: 88 NQNIIIFNSVFLD-----FSVFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIR 141
 Sbjct: 852 NQSISFSNDFFENGTLNSFSIYFWLR--NLGKDITKS-----KLIGSKEDNCGWEIYFQ 903
 Query: 142 GNRIIWTLIDINGKTGSVFFEYNIREDISEYINRWFFVTITNN--LNNAKIYINGKLESN 199
 Sbjct: 904 DTGLVFNMIDSNGNEKNIYL-----SDVSN--NSWHYITISVDRLKEQLLIFIDDNLVAN 956
 Query: 200 TDIKDIREVIANGEIIFKLDGIDRTQFIWMKYFSIFNTELSOSNIEERYKIQSYSEYLK 259
 Sbjct: 957 ESIKEILNIYSSNTISL-----VDENNPIYVEGLSILNKPTTSQEVLNSYFKVLNNSYIR 1011
 Query: 260 DFWGNPLMYNKEYYMFN-----AGKNNSYIKLKKDSPVGEILTRSK---YNQNS 305
 Sbjct: 1012 DSSEERLEYNKTYQLYNYVFSENPIYEIKQNNNIYLTINNTNNLNQVSFKLLSINPNK 1071
 Query: 306 KYINYRDLYI-----GEKFI-IRRKSNSQSINDDIVRKEDYIYLDFFNLN 349
 Sbjct: 1072 QYVQKLDEVIISVLDNMEKYIDISEDNRLQLIDNKNNAKKMIISNDIFISN 1122

Query: 306 KYINYRDLYI-----GEKFI-IRRKSNSQSINDDIVRKEDYIYLDFFNLN 349
 +Y+ D I EK+I I + Q I++ K+ I D F N
 Sbjct: 1104 QYVQKLDEVIISVLDNMEKYIDISEDNRQLIDNKNNAKKMIISNDIFISN 1154

tr 069276 **Nontoxic-nonhaemagglutinin [ntnh] [Clostridium** 1161
069276_CLOBO **botulinum]** AA
align

Score = 68.9 bits (167), Expect = 2e-10
 Identities = 69/291 (23%), Positives = 127/291 (42%), Gaps = 49/291 (16%)

Query: 88 NQNIIIFNSVFLD-----FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSWKISIR 141
 NQ+I F++ F + FS+ FW+R D I++ +I ++N GW+T +
 Sbjct: 852 NQSISFSNDFFENGTLNSFSIYFWLR--NLGKDTIKS-----KLIGSKEDNCGWEIYFQ 903

Query: 142 GNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNN--LNNAKIYINGKLESN 199
 +++ +ID NG .K+++ D+S N W ++T+ + T+T+ L +N
 Sbjct: 904 DTGLVFNMIDSNGNEKNIYL----SDVSN--NSWHYITISVDRLKEQLLIFIDDNLVAN 956

Query: 200 TDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNSIEERYKIQSSEYLK 259
 IK+I + ++ I + + SI N + + Y + Y++
 Sbjct: 957 ESIKEILNIYSSNTISL----VNENNPYVEGLSILNKPTTSQEVLNSYFKVLNNSYIR 1011

Query: 260 DFWGNPLMYNKEYYMFN-----AGNKNSYIKLKKDSPVGEILTRSK---YNQNS 305
 D L YNK Y ++N N N Y+ + + + +++ K N N
 Sbjct: 1012 DSSEERLEYNKTYQLYNVFSENPIYEIKQNNNIYLTTINNTNNLNLQVSKFKLLSINPNK 1071

Query: 306 KYINYRDLYI-----GEKFI-IRRKSNSQSINDDIVRKEDYIYLDFFNLN 349
 +Y+ D I EK+I I + Q I++ K+ I D F N
 Sbjct: 1072 QYVQKLDEVIISVLDNMEKYIDISEDNRQLIDNKNNAKKMIISNDIFISN 1122

tr Q45887 **Botulinum neurotoxin type F nontoxic-nonhemagglutinin** 1165
Q45887_CLOBO **component [ntnh]** AA
[Clostridium botulinum] align

Score = 67.8 bits (164), Expect = 5e-10
 Identities = 80/328 (24%), Positives = 143/328 (43%), Gaps = 58/328 (17%)

Query: 45 KDNNLI-DLSGYGAKVEVYDGVELNDKNQFKLTSSANSKIRVT-QNQNIIFNSVFLD--- 99
 +ENN+I D SG V+ G+EL + NS + + NQ+IIF + + +
 Sbjct: 813 QDNNVIGDASGKNTLVEYPKGIEL-----VYGINNSALYLNQNSQSIIFTNDYFENGL 865

Query: 100 ---FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSWKISIRGNRIIWTLIDINGKT 156
 FS+ FW+R N Q+ I ++ +T + N GW+T + ++ +ID NG
 Sbjct: 866 TNSFSIYFWLR----NLG-QDTIKSK--LIGSKEYNCGWEIYFQEIGHVFNMIDSNGNE 917

Query: 157 KSVFFEYNIREDISEYINRWFFVTITNN--LNNAKIYINGKLESNTDIKDIREVIANGEI 214
 K++ D+S N W ++T+ + T+T+ L N IKDT + ++ I
 Sbjct: 918 KNIYL----SDVSN--NSWHYITISVDRLKEQLLIFIDDNLVNVNESIKDILNIYSSNII 970

Query: 215 IFKLDGDIDRTQFIWMKYFSIFNTELSQSNSIEERYKIQSSEYLKDFWGNPLMYNKEYYM 274
 D + ++ +I N + + Y + Y++D L YNK Y +

Query: 306 KYINYRDLYI-----GEKFI-IRRKSNSQSINDDIVRKEDYIYLDFFNLN 349
 +Y+ D I EK+I I + Q I++ K+ I D F N
 Sbjct: 1104 QYVQKLDEVIISVLNDNMEKYIDISEDNRLQLIDNKNNAKKMIISNDIFISN 1154

tr 069276 **Nontoxic-nonhaemagglutinin [ntnh] [Clostridium** 1161
069276_CLOBO **botulinum]** AA
align

Score = 68.9 bits (167), Expect = 2e-10
 Identities = 69/291 (23%), Positives = 127/291 (42%), Gaps = 49/291 (16%)

Query: 88 NQNIIFNSVFLD-----FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSWKISIR 141
 NQ+I F++ F + FS+ FW+R D I++ +I ++N GW+I +
 Sbjct: 852 NQSIISFSNDFFENGTLNSFSIYFWLR--NLGKDTIKS-----KLIGSKEDNCGWEIYFQ 903

Query: 142 GNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNN--LNNAKIYINGKLESN 199
 ++++ +ID NG K+++ D+S N W ++T+ + T+I+ L +N
 Sbjct: 904 DTGLVFNMIDSNGNEKNIYL----SDVSN--NSWHYITISVDRLKEQLLIFIDDNLVAN 956

Query: 200 TDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNSIEERYKIQSSEYLK 259
 .IK+I + ++ I + + I++ SI N + + Y + Y++
 Sbjct: 957 ESIKEILNIYSSNTISL----VNENNPIYVEGLSILNKPTTSQEVLNSYFKVLNNSYIR 1011

Query: 260 DFWGNPLMYNKEYYMFN-----AGNKNSYIKLKKDSPVGEILTRSK---YNQNS 305
 D L YNK Y ++N N N Y+ + + + +++ R N N
 Sbjct: 1012 DSSEERLEYNKTYQLYNYVFSENPIYEIKQNNNIYLTINNTNNLNQVSKFKLLSINPNK 1071

Query: 306 KYINYRDLYI-----GEKFI-IRRKSNSQSINDDIVRKEDYIYLDFFNLN 349
 +Y+ D I EK+I I + Q I++ K+ I D F N
 Sbjct: 1072 QYVQKLDEVIISVLNDNMEKYIDISEDNRLQLIDNKNNAKKMIISNDIFISN 1122

tr Q45887 **Botulinum neurotoxin type F nontoxic-nonhemagglutinin** 1165
Q45887_CLOBO **component [ntnh]** AA
[Clostridium botulinum] align

Score = 67.8 bits (164), Expect = 5e-10
 Identities = 80/328 (24%), Positives = 143/328 (43%), Gaps = 58/328 (17%)

Query: 45 KDNNLI-DLSGYGAKVEVYDGVELNDKNQFKLTSSANSKIRVT-QNQNIIFNSVFLD--- 99
 +DNN+I D SG VE G+EJ + NS + + NQ+IIF + + +
 Sbjct: 813 QDNNVIGDASGKNTLVEYPKGIEL-----VYGINNSALYLNQSNQSIIFTNDYFENGL 865

Query: 100 ---FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSWKISIRGNRIIWTLIDINGKT 156
 FS+ FW+R N G Q+ I ++ +I + N GW+I + ++ +ID NG
 Sbjct: 866 TNSFSIYFWLR----NLG-QDTIKSK--LIGSKEYNCGWEIYFQEIGHVFNMIDSNGNE 917

Query: 157 KSVFFEYNIREDISEYINRWFFVTITNN--LNNAKIYINGKLESNTDIKDIREVIANGEI 214
 K+++ D+S N W ++T+ + T+I+ L N IKDT + ++ I
 Sbjct: 918 KNIYL----SDVSN--NSWHYITISVDRLKEQLLIFIDDNLVNVESIKDILNIYSSNII 970

Query: 215 IFKLDGDIDRTQFIWMKYFSIFNTELSQSNSIEERYKIQSSEYLKDFWGNPLMYNKEYYM 274
 D + ++ +I N + + Y + Y++D L YNK Y +

Sbjct: 971 SLLSDNKAS----YIEGLTILNKPTTGEELRNYFKNLNNNSYVRDSNDERLEYNKTYQL 1025
 Query: 275 FN-AGNKNSYIKLKKDSPVGEILTR-----SKYNQNSKYINYRD----LY 314
 ++ N ++K+D+ + + N N +Y+ D LY
 Sbjct: 1026 YDYVFPDNPICEVKQDNNIYLTIINNINNLMKPCFKLLSINSNKQYVQWKDEVIVSLY 1085
 Query: 315 IGEKFI-IRRKSNSQSINDDIVRKEDYI 341
 EK++ I ++N I D+ + + +
 Sbjct: 1086 DTEKYVCISNENNRRVIIDNKIMQVKFI 1113

tr Q45844 Neurotoxin complex M nontoxic-nonhemagglutinin 1165
Q45844_CLOBO component [NTNH] AA
 [Clostridium botulinum] align

Score = 67.8 bits (164), Expect = 5e-10
 Identities = 80/328 (24%), Positives = 143/328 (43%), Gaps = 58/328 (17%)

Query: 45 KDNNLII-DLSGYGAKVEVYDGVELNDKNQFKLTSSANSKIRVT-QNQNIIFNSVFLED--- 99
 +DNNN+I D SG VE G+EL + NS + + NQ+IIF + + +
 Sbjct: 813 QDNNVIGDASGKNTLVEYPKGIEL-----VYGINNSALYLNGSNQSIIFTNDYFENGL 865

Query: 100 ---FSVSEFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKT 156
 FS+ FW+R N G Q+ I ++ +I + N GW+I + + + ID NG
 Sbjct: 866 TNSFSIYFWLR----NLG-QDTIKSK--LIGSKEYNCGWEIYFQEIGHVFNMDNGNE 917

Query: 157 KSVFFEYNIREDISEYINRWFFVTITNN--LNNAKIYINGKLESNTDIKDIREVIANGEI 214
 K+++ D+S N W ++T+ + + I+I+ L N IKDI + ++ I
 Sbjct: 918 KNIYL----SDVSN--NSWHYITISVDRLKEQLLIFIDDNLVVNESIKDILNIYSSNII 970

Query: 215 IFKLDGDIDRTQFIFWMKYFSIFNTELSQSNIIEERYKIQSYSSEYLKDFWGPNPLMYNKEYYM 274
 D +++ +T N + + Y + Y++D L YNN Y +
 Sbjct: 971 SLLSDNKAS----YIEGLTILNKPTTGEELRNYFKNLNNNSYVRDSNDERLEYNKTYQL 1025

Query: 275 FN-AGNKNSYIKLKKDSPVGEILTR-----SKYNQNSKYINYRD----LY 314
 ++ N ++K+D+ + + N N +Y+ D LY
 Sbjct: 1026 YDYVFPDNPICEVKQDNNIYLTIINNINNLMKPCFKLLSINSNKQYVQWKDEVIVSLY 1085

Query: 315 IGEKFI-IRRKSNSQSINDDIVRKEDYI 341
 EK++ I ++N I D+ + + +
 Sbjct: 1086 DTEKYVCISNENNRRVIIDNKIMQVKFI 1113

tr Q564H3 Neurotoxin heavy chain [Clostridium sp. 167 AA
Q564H3_9CLOT RKD] align

Score = 63.5 bits (153), Expect = 9e-09
 Identities = 50/167 (29%), Positives = 71/167 (41%), Gaps = 13/167 (7%)

Query: 301 YNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFNLNQEWRYXXXX 360
 Y I YR LY G KFTI+R + + I D V+ D+I L N E V
 Sbjct: 9 YTNGKLNIYYRRLYNGLKFIIKRYTPNNEI-DSFVKSGDFIKLYVSYNNEHIVGYPKDG 67

Query: 361 XXXXXXXXXXXXAPI---SDSDEFYNTIQIKEYDEQPTYSQQLFFKDEESTDEIGLIGHRF 417
 + + Y ++ + * TYS QI D+ ++ +GL+G X

Sbjct: 971 SLLSDNKAS-----YIEGLTILNKPTTGEEVLRNYFKNLNNNSYVRDSNDERLEYNKTYQL 1025

Query: 275 FN-AGNKNSYIKLKKDSPVGEILTR-----SKYNQNSKYINYRD----LY 314
 ++ N ++K+D+ + + N N +Y+ D LY

Sbjct: 1026 YDYVFPDPNPICEVKQDNNIYLTIINNINNLMKPCFKLLSINSNKQYVQKWDEVIISVLY 1085

Query: 315 IGEKFI-IRRKSNSQSINDDIVRKEDYI 341
 EK++ I ++N I D+ + + +I

Sbjct: 1086 DTEKYVCISNENNRVKIIDNKIMQVKFI 1113

tr Q56844 Neurotoxin complex M nontoxic-nonhemagglutinin 1165
Q56844_CLOBO component [NTNH] AA
 [Clostridium botulinum] align

Score = 67.8 bits (164), Expect = 5e-10
 Identities = 80/328 (24%), Positives = 143/328 (43%), Gaps = 58/328 (17%)

Query: 45 KDNNLII-DLSGYGAKVEVYDGVELNDKNQFKLTSSANSKIRVT-QNQNIIFNSVFLD--- 99
 +DNNN+I D SG VS G+EL + NS + + NQ+HIF + + +

Sbjct: 813 QDNNVIGDASGKNTLVEYPKGIEL-----VYGINNSALYNGSNQSIIFTNDYFENGL 865

Query: 100 ---FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKT 156
 FS+ FW+R N G Q+ I ++ +I + N GW+I + ++ +ID NG

Sbjct: 866 TNSFSIYFWLR----NLG-QDTIKSK--LIGSKEYNCGWEIYFQEIGHVFNMIDSNGNE 917

Query: 157 KSVFFEYNIREDISEYINRWFFVTITNN--LNNAKIYINGKLESNTDIKDIREVIANGEI 214
 K+++ D+S N W ++T+I+ + I+I+ L N IKDI + ++ I

Sbjct: 918 KNIYL----SDVSN--NSWHYITISVDRLKEQLLIFIDDNLVVNESIKDILNIYSSNII 970

Query: 215 IFKLDGDIDRTQFIWMKYFSIFNTELSQSNIIEERYKIQSYSEYLKDFWGNPLMYNKEYYM 274
 D +++ +T N + + Y + Y++D L YNN Y +

Sbjct: 971 SLLSDNKAS-----YIEGLTILNKPTTGEEVLRNYFKNLNNNSYVRDSNDERLEYNKTYQL 1025

Query: 275 FN-AGNKNSYIKLKKDSPVGEILTR-----SKYNQNSKYINYRD----LY 314
 ++ N ++K+D+ + + N N +Y+ D LY

Sbjct: 1026 YDYVFPDPNPICEVKQDNNIYLTIINNINNLMKPCFKLLSINSNKQYVQKWDEVIISVLY 1085

Query: 315 IGEKFI-IRRKSNSQSINDDIVRKEDYI 341
 EK++ I ++N I D+ + + +I

Sbjct: 1086 DTEKYVCISNENNRVKIIDNKIMQVKFI 1113

tr Q564H3 Neurotoxin heavy chain [Clostridium sp. 167 AA
Q564H3_9CLOT RKD] align

Score = 63.5 bits (153), Expect = 9e-09
 Identities = 50/167 (29%), Positives = 71/167 (41%), Gaps = 13/167 (7%)

Query: 301 YNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYXXXX 360
 Y I YR LY G KFTI+R + + T D V+ D+I L N E V

Sbjct: 9 YTNGKLNIIYRRLYNGLKFIIKRYTPNNEI-DSFVKSGDFIKLYVSYNNNEHIVGYPKDG 67

Query: 361 XXXXXXXXXXXXAPI---SDSDEFYNTIQIKEYDEQPTYSQCQLFKKDEESTDEIGLIGHRF 417
 + * Y ++ + + TYS QI D+ ++ +GL+G H

Sbjct: 68 NAFNNLDRILRVGYNAPGIPLYKKMEAVKLRDLKTVQLKLYDDKNAS--LGLVGTHN- 124
 Query: 418 YESGIVFEEYKDYFCISKWYLKEVKRKPYNLKGNCNWQFIPKDEGWT 464
 I + +D S WY +K K LGC+W F+F DEGWT
 Sbjct: 125 --GQIGNDPNRDILIASNWFNHLDKI---LGCDWYFVPTDEGWT 165

tr Q9ZAJ6 **Ntnh protein [ntnh] [Clostridium botulinum]** 1162 AA
Q9ZAJ6_CLOBO align

Score = 63.5 bits (153), Expect = 9e-09
 Identities = 70/293 (23%), Positives = 124/293 (41%), Gaps = 53/293 (18%)

Query: 88 NQNIIFNSVFLD-----FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIR 141
 NQ+I F++ F + FS+ FW+R N G + +I ++N GW+I +
 Sbjct: 849 NQSISFSNDFFENGTLTNSFSIHFWR-----NLGQDT---TKSKLIGSKEDNCGWEIYFQ 900
 Query: 142 GNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNN--LNNAKIYINGKLESN 199
 +++ +ID NG K+++ D+S N W ++TI+ + T+I+ L N
 Sbjct: 901 NTGLVFNMIDSNGDEKNIYL----SDVSN--NSWHYITISVDRLKEQLLIFIDDNLVVN 953
 Query: 200 TDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIIEERYKIQSYSEYLK 259
 IK+I + ++ I D + +++ +I N + + Y + Y++
 Sbjct: 954 ESIKEILNIYSSNIISLLSDNNAS----YIEGLTILNKPTTGEEVLSNYFKNLNNSYIR 1008
 Query: 260 DFWGNPLMYNKEYYMFN-----AGNKN SYIKLKKDSPVGEILTRSKY----NQ 303
 D L YNK Y ++N N N Y+ + + + L SK+ N
 Sbjct: 1009 DSNEERLEYNKTYQLYNVFSDKPICEVKQNNNIYLTTINNTNNLN--LQASKFKLLSINP 1066
 Query: 304 NSKYINYRDLYI-----GEKFI-IRRKSNSQSINDDIVRKEDYIYLDFFNLN 349
 N +Y+ D I EK+I I + Q I++ K+ I D F N
 Sbjct: 1067 NKQYVQKFDEVIISVLDNMEKYIDISEDNRQLIDNKNSAKKMIISNDIFISN 1119

tr Q45914 **Type A progenitor toxin nontoxic-nonHA (NTNH) [ant]** 1193
Q45914_CLOBO **[Clostridium botulinum]** AA
align

Score = 63.2 bits (152), Expect = 1e-08
 Identities = 69/293 (23%), Positives = 125/293 (42%), Gaps = 53/293 (18%)

Query: 88 NQNIIFNSVFLD-----FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIR 141
 NQ+I F++ F + FS+ FW+R D T++ +I ++N GW+I +
 Sbjct: 884 NQSISFSNDFFENGTLTNSFSIYFWLR--NLGKDTIKS-----KLIGSKEDNCGWEIYFQ 935
 Query: 142 GNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNN--LNNAKIYINGKLESN 199
 +++ +ID NG K+++ D+S N W ++TI+ + I+I+ L N
 Sbjct: 936 DTGLVFNMIDSNGNEKNIYL----SDVSN--NSWHYITISVDRLKEQLLIFIDDNLVAN 988
 Query: 200 TDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIIEERYKIQSYSEYLK 259
 IK+I + ++ I + +++ +I N + + Y + Y++
 Sbjct: 989 ESIKEILNIYSSNIISL----LSENNPSYIEGLTILNKPTTSQEVLNSYFEVLNNSYIR 1043
 Query: 260 DFWGNPLMYNKEYYMFN-----AGNKN SYIKLKKDSPVGEILTRSKY----NQ 303
 D I YNK Y ++N N N Y+ + + + L SK+ N

Sbjct: 68 NAFNNLDRILRVGYNAPGIPLYKKMEAVKLRDLKTVQLKLYDDKNAS--LGLVGTHN- 124

Query: 418 YESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWT 464

I + +D S WY +K K LGC+W F+P DEGWT

Sbjct: 125 --GQIGNDPNRDILIASNWYFNHLKDKI----LGCDWYFVPTDEGWT 165

tr Q9ZAJ6 **Ntnh protein [ntnh] [Clostridium botulinum]** 1162 AA
Q9ZAJ6_CLOBO align

Score = 63.5 bits (153), Expect = 9e-09

Identities = 70/293 (23%), Positives = 124/293 (41%), Gaps = 53/293 (18%)

Query: 88 NQNIIFNSVFLD-----FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIR 141
NQ+I F++ F + FS+ FW+R N G + +I ++N GW+I +

Sbjct: 849 NQSISFSNDFFENGTLNSFSIHFWR-----NLGQDT---TKSKLIGSKEDNCGWEIYFQ 900

Query: 142 GNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNN--LNNAKIYINGKLESN 199
+++ +ID NG K+++ D+S N W ++TT+ + I+I+ L N

Sbjct: 901 NTGLVFNMDNSNGDEKNIYL----SDVSN--NSWHYITISVDRLKEQLLIFIDDNLVVN 953

Query: 200 TDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIIEERYKIQSYSEYLK 259
IK+I + ++ I D + +++ +I N + + Y + Y++

Sbjct: 954 ESIKEILNIYSSNIISLLSDNNAS-----YIEGLTILNKPTTGEEVLSNYFKNLNNSYIR 1008

Query: 260 DFWGNPLMYNKEYYMFN-----AGNKNSYIKLKKDSPVGEILTRSKY----NQ 303
D L YNK Y ++N N N Y+ + + + L SK+ N

Sbjct: 1009 DSNEERLEYNKTYQLYNVFSDKPICEVKQNNNIYLTINNTNNLN--LQASKFKLLSINP 1066

Query: 304 NSKYINYRDLYI-----GEKFI-IRRKSNSQSINDDIVRKEDYIYLDFFNLN 349
N +Y+ D I EK+I I + Q I++ R+ I D F N

Sbjct: 1067 NKQYVQKFDEVIIISVLDNMEKYIDISEDNRQLIDNKNSAKKMIISNDIFISN 1119

tr Q45914 **Type A progenitor toxin nontoxic-nonHA (NTNH) [ant]** 1193
Q45914_CLOBO **[Clostridium botulinum]** AA align

Score = 63.2 bits (152), Expect = 1e-08

Identities = 69/293 (23%), Positives = 125/293 (42%), Gaps = 53/293 (18%)

Query: 88 NQNIIFNSVFLD-----FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIR 141
NQ+I F++ F + FS+ FW+R D T++ +I ++N GW+I +

Sbjct: 884 NQSISFSNDFFENGTLNSFSIYFWRL--NLGKDTIKS-----KLIGSKEDNCGWEIYFQ 935

Query: 142 GNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNN--LNNAKIYINGKLESN 199
+++ +ID NG K+++ D+S N W ++TT+ + I+I+ L +N

Sbjct: 936 DTGLVFNMDNSNGNEKNIYL----SDVSN--NSWHYITISVDRLKEQLLIFIDDNLVAN 988

Query: 200 TDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIIEERYKIQSYSEYLK 259
IK+I + ++ I + + +++ +I N + + Y + Y++

Sbjct: 989 ESIKEILNIYSSNIISL-----LSENNPSYIEGLTILNKPTTSQEVLNSYFEVLNNSYIR 1043

Query: 260 DFWGNPLMYNKEYYMFN-----AGNKNSYIKLKKDSPVGEILTRSKY----NQ 303
D L YNK Y ++N N N Y+ + + + L SK+ N

Sbjct: 1044 DSNEERLEYNKTYQLYNVFSKPKICEVKQNNNIYLTTINNTNNLN--LQASKFKLLSINP 1101
 Query: 304 NSKYINYRDLYI-----GEKFI-IRRKSNSQSINDDIVRKEDYIYLDFNLN 349
 N +Y+ D I EK+I I + Q I++ K+ I D F N
 Sbjct: 1102 NKQYVQKLDEVIISVLDNMEKYIDISEDNRLQLIDNKNNAKKMIISNDIFISN 1154

tr P71107 **Ntnh protein [ntnh] [Clostridium botulinum]** 1193 AA
P71107_CLOBO **A]** align
 Score = 63.2 bits (152), Expect = 1e-08
 Identities = 69/293 (23%), Positives = 125/293 (42%), Gaps = 53/293 (18%)
 Query: 88 NQNIIFNSVF-----FSVFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSWKISIR 141
 NQ+I F++ F + FS+ FW+R D I++ +I ++N GW+I +
 Sbjct: 884 NQSISFSNDFFENGTLNSFSIYFWLR--NLGKDTIKS-----KLIGSKEDNCGWEIYFQ 935
 Query: 142 GNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNN--LNNAKIYINGKLESN 199
 +++ +ID NG K+++ D+S N W ++T+ + T+I+ L +N
 Sbjct: 936 DTGLVFNMIDSNGNEKNIYL----SDVSN--NSWHYITISVDRLKEQLLIFIDDNLVAN 988
 Query: 200 TDIDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTLSQSNEERYKIQSSEYLK 259
 IK+I + ++ I + + + +I N + + Y + Y++
 Sbjct: 989 ESIKEILNIYSSNIISL----LSENNPSYIEGLTILNKPTTSQEVLNSYFEVLNNSYIR 1043
 Query: 260 DFWGNPLMYNKEYYMFN-----AGNKNSYIKLKKDSPVGEILTRSKY----NQ 303
 D L YNK Y ++N N N Y+ + + L SK+ N
 Sbjct: 1044 DSNEERLEYNKTYQLYNVFSKPKICEVKQNNNIYLTTINNTNNLN--LQASKFKLLSINP 1101
 Query: 304 NSKYINYRDLYI-----GEKFI-IRRKSNSQSINDDIVRKEDYIYLDFNLN 349
 N +Y+ D I EK+I I + Q I++ K+ I D F N
 Sbjct: 1102 NKQYVQKLDEVIISVLDNMEKYIDISEDNRLQLIDNKNNAKKMIISNDIFISN 1154

tr Q45850 **Ntnh protein [ntnh] [Clostridium botulinum]** 1163 AA
Q45850_CLOBO **A]** align
 Score = 62.8 bits (151), Expect = 2e-08
 Identities = 49/214 (22%), Positives = 100/214 (45%), Gaps = 29/214 (13%)
 Query: 88 NQNIIFNSVF-----FSVFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSWKISIR 141
 NQ+I F++ F + FS+ FW+R D I++ +I ++N GW+I +
 Sbjct: 850 NQSISFSNDFFENGTLNSFSIYFWLR--NLGKDTIKS-----KLIGSKEDNCGWEIYFQ 901
 Query: 142 GNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNN--LNNAKIYINGKLESN 199
 +++ +ID NG K+++ D+S N W ++T+ + T+I+ L N
 Sbjct: 902 DTGLVFNMIDSNGNEKNIYL----SDVSN--NSWHYITISIDRLKEQLLIFIDDNLVAN 954
 Query: 200 TDIDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTLSQSNEERYKIQSSEYLK 259
 IK+I + ++ I + + + +I N + + Y + Y++
 Sbjct: 955 ESIKEILNIYSSNIISL----LSNNNASYIEGLTILNKPTTSQEVLNSYFKNLNNSYIR 1009
 Query: 260 DFWGNPLMYNKEYYMFN-AGNKNSYIKLKKDSPV 292
 D L YNK Y ++N ++N ++K++ +
 Sbjct: 1010 DSNEERLEYNKTYQLYNVFSENPIYEIKQNNNI 1043

Sbjct: 1044 DSNEERLEYNKTYQLYNYVFSDKPICEVKQNNNIYLTIINNTNNLN--LQASKFKLLSINP 1101
 Query: 304 NSKYINYRDLYI-----GEKFI-IRRKSNSQSINDDIVRKEDYIYLDFFNLN 349
 N +Y+ D I EK+E I + Q I++ K+ I D F N
 Sbjct: 1102 NKQYVQKLDEVIISVLDNMEKYIDISEDNRLQLIDNKNNAKKMIISNDIFISN 1154

tr P71107 **Ntnh protein [ntnh] [Clostridium botulinum]** 1193 AA
P71107_CLOBO **A]** align
 Score = 63.2 bits (152), Expect = 1e-08
 Identities = 69/293 (23%), Positives = 125/293 (42%), Gaps = 53/293 (18%)
 Query: 88 NQNIIFNSVFLD-----FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSWKISIR 141
 NQ+I F++ F + F+S F W+R D I++ +I ++N GW+I +
 Sbjct: 884 NQSISFSNDFFENGTLTNSFSIYFWLR--NLGKDTIKS-----KLIGSKEDNCGWEIYFQ 935
 Query: 142 GNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNN--LNNAKIYINGKLESN 199
 +++ +ID NG K+++ D+S N W ++TI+ + I+I+ L +N
 Sbjct: 936 DTGLVFNMIDSNGNEKNIYL----SDVSN--NSWHYITISVDRLKEQLLIFIDDNLVAN 988
 Query: 200 TDIKDIREVIANGEIIIFKLDGDIDRTQFIWMKYFSIFNTLSQSNIIEERYKIQSYSEYLK 259
 IK+I + ++ I + + + +I N + + Y + Y++
 Sbjct: 989 ESIKEILNIYSSNIISL----LSENNPSYIEGLTILNKPTTSQEVLNSYFEVLNNSYIR 1043
 Query: 260 DFWGNPLMYNKEYYMFN-----AGNKNSYIKLKKDSPVGEILTRSKY----NQ 303
 D L YNK Y ++N N N Y+ + + + L SK+ N
 Sbjct: 1044 DSNEERLEYNKTYQLYNYVFSDKPICEVKQNNNIYLTIINNTNNLN--LQASKFKLLSINP 1101
 Query: 304 NSKYINYRDLYI-----GEKFI-IRRKSNSQSINDDIVRKEDYIYLDFFNLN 349
 N +Y+ D I EK+E I + Q I++ K+ I D F N
 Sbjct: 1102 NKQYVQKLDEVIISVLDNMEKYIDISEDNRLQLIDNKNNAKKMIISNDIFISN 1154

tr Q45850 **Ntnh protein [ntnh] [Clostridium botulinum]** 1163 AA
Q45850_CLOBO
 align
 Score = 62.8 bits (151), Expect = 2e-08
 Identities = 49/214 (22%), Positives = 100/214 (45%), Gaps = 29/214 (13%)
 Query: 88 NQNIIFNSVFLD-----FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSWKISIR 141
 NQ+I F++ F + F+S F W+R D I++ +I ++N GW+I +
 Sbjct: 850 NQSISFSNDFFENGTLTNSFSIYFWLR--NLGKDTIKS-----KLIGSKEDNCGWEIYFQ 901
 Query: 142 GNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNN--LNNAKIYINGKLESN 199
 +++ +ID NG K+++ D+S N W ++TI+ + I+I+ L N
 Sbjct: 902 DTGLVFNMIDSNGNEKNIYL----SDVSN--NSWHYITISIDRLKEQLLIFIDDNLVAN 954
 Query: 200 TDIKDIREVIANGEIIIFKLDGDIDRTQFIWMKYFSIFNTLSQSNIIEERYKIQSYSEYLK 259
 IK+I + ++ I + + + +I N + + Y + Y++
 Sbjct: 955 ESIKEILNIYSSNIISL----LSNNNASYIEGLTILNKPTTSQEVLNSYFKNLNNSYIR 1009
 Query: 260 DFWGNPLMYNKEYYMFN-AGNKNSYIKLKKDSPV 292
 D L YNK Y ++N ++N ++K+ ++ +
 Sbjct: 1010 DSNEERLEYNKTYQLYNYVSENPIYEIKQNNNI 1043

tr P71108 Nontoxic-nonhemagglutinin component [Clostridium botulinum] 1193
P71108_CLOBO AA align

Score = 61.6 bits (148), Expect = 3e-08
 Identities = 69/293 (23%), Positives = 124/293 (41%), Gaps = 53/293 (18%)

Query: 88 NQNIIFNSVFLD-----FSVSEWIRIPKYKNDGIQNYIHNEYTIINCMKNNSWKISIR 141
 NQ+I F++ F + FS+ FW+R D I++ Y+I +N GW+I +
 Sbjct: 884 NQSISFSNDFFENGLTNSFSIYFWLR--NLGKDTIKS-----KLIGSKGDNCGWEIYFQ 935

Query: 142 GNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNN--LNNAKIYINGKLESN 199
 +++ +ID NG K+++ D+S N W ++T+ + I+I+ L +N
 Sbjct: 936 DTGLVFNMIDSNGNEKNIYL----SDVSN--NSWHYITISVDRLKEQLLIFIDDNLVAN 988

Query: 200 TDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSSEYLK 259
 IK+I + ++ I + + + + I N + + Y + Y++
 Sbjct: 989 ESIKEILNIYSSNIISL----LSENNPSYIEGLTILNKPTTSQEVLNNYFKVLNNSYIR 1043

Query: 260 DFWGNPLMYNKEYYMFN-----AGNKNSYIKLKKDSPVGEILTRSKY----NQ 303
 D L YNK Y +N N N Y+ + + + L SK+ N
 Sbjct: 1044 DSNEERLEYNKTYQLNYVFSDKPICEVKQNNNIYLTINNTNNLN--LQPSKFKLLSINP 1101

Query: 304 NSKYINYRDLYI-----GEKFI-IRRKSNSQSINDDIVRKEDYIYLDFFNLN 349
 N +Y+ D I EK+I I + Q I++ K+ I D F N
 Sbjct: 1102 NKQYVQKLDEVIISVLGNMEKYIDISEDNRQLIDNKNGAKMIIISNDMFISN 1154

tr P71109 Nontoxic-nonhemagglutinin [ntnh] [Clostridium botulinum] 1159
P71109_CLOBO AA align

Score = 61.2 bits (147), Expect = 5e-08
 Identities = 69/293 (23%), Positives = 125/293 (42%), Gaps = 53/293 (18%)

Query: 88 NQNIIFNSVFLD-----FSVSEWIRIPKYKNDGIQNYIHNEYTIINCMKNNSWKISIR 141
 NQ+I F++ F + FS+ FW+R D I+ Y+I +N GW+I +
 Sbjct: 850 NQSISFSNDFFENGLTNSFSIYFWLR--NLGKDTIK-----YKLIGSKEDNCGWEIYFQ 901

Query: 142 GNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNN--LNNAKIYINGKLESN 199
 +++ +ID NG K+++ D+S N W ++T+ + I+I+ L +N
 Sbjct: 902 DTGLVFNMIDSNGNEKNIYL----SDVSN--NSWHYITISVDRLKEQLLIFIDDNLVAN 954

Query: 200 TDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSSEYLK 259
 IK+I + ++ I + + + + I N + + Y + Y++
 Sbjct: 955 ESIKEILNIYSSNIISL----LSENKPSYIEGLTILNKPTTSQEVLNNYFKVLNNSYIR 1009

Query: 260 DFWGNPLMYNKEYYMFN-----AGNKNSYIKLKKDSPVGEILTRSKY----NQ 303
 D L Y+K Y + N N N Y+ + + + L SK+ N
 Sbjct: 1010 DSNEERLEYHKTYQLDNYVFSDKPICEVKQNNNIYLTINNTNNLN--LQPSKFKLLSINS 1067

Query: 304 NSKYINYRDLYI-----GEKFI-IRRKSNSQSINDDIVRKEDYIYLDFFNLN 349
 N +Y+ D I EK+I I + Q I++ K+ I D F N

tr P71108 Nontoxic-nonhemagglutinin component [Clostridium botulinum] 1193
P71108_CLOBO AA
align

Score = 61.6 bits (148), Expect = 3e-08
 Identities = 69/293 (23%), Positives = 124/293 (41%), Gaps = 53/293 (18%)

Query: 88 NQNIIFNSVFLD-----FSVFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIR 141
 NQ+I F++ F + FS+ FW+R D T++ Y+I ++N GW+I +
 Sbjct: 884 NQSISFSNDFFENGTLNSFSIYFWLR--NLGKDTIKS-----KLIGSKGDNCGWEIYFQ 935

Query: 142 GNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNN--LNNAKIYINGKLESN 199
 +++ +ID NG K+++ D+S N W ++T+ + I+I+ L +N
 Sbjct: 936 DTGLVFNMIDSNGNEKNIYL----SDVSN--NSWHYITISVDRLKEQLLIFIDDNLVAN 988

Query: 200 TDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNEERYKIQSSEYLK 259
 IK+I + ++ I + + + +T N + + Y + Y++
 Sbjct: 989 ESIKEILNIYSSNIISL----LSENNPSYIEGLTILNKPTTSQEVLNNYFKVLNNSYIR 1043

Query: 260 DFWGNPLMYNKEYYMFN-----AGNKNSYIKLKKDSPVGEILTRSKY----NQ 303
 D L YNK Y +N N N Y+ + + + L SK+ N
 Sbjct: 1044 DSNEERLEYNKTYQLNYVFSDKPICEVKQNNNIYLTINNTNNLN--LQPSKFKLLSINP 1101

Query: 304 NSKYINYRDLYI-----GEKFI-IRRKSNSQSINDDIVRKEDYIYLDFFNLN 349
 N +Y+ D I EK+I I + Q I++ K+ I D F N
 Sbjct: 1102 NKQYVQKLDEVIISVLGNMEKYIDISEDNRQLIDNKNGAKMIIISNDMFISN 1154

tr P71109 Nontoxic-nonhemagglutinin [ntnh] [Clostridium botulinum] 1159
P71109_CLOBO AA
align

Score = 61.2 bits (147), Expect = 5e-08
 Identities = 69/293 (23%), Positives = 125/293 (42%), Gaps = 53/293 (18%)

Query: 88 NQNIIFNSVFLD-----FSVFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIR 141
 NQ+I F++ F + FS+ FW+R D T++ Y+I ++N GW+I +
 Sbjct: 850 NQSISFSNDFFENGTLNSFSIYFWLR--NLGKDTIK-----YKLIGSKEDNCGWEIYFQ 901

Query: 142 GNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNN--LNNAKIYINGKLESN 199
 +++ +ID NG K+++ D+S N W ++T+ + T+T+ L +N
 Sbjct: 902 DTGLVFNMIDSNGNEKNIYL----SDVSN--NSWHYITISVDRLKEQLLIFIDDNLVAN 954

Query: 200 TDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNEERYKIQSSEYLK 259
 IK+I + ++ I + + + +T N + + Y + Y++
 Sbjct: 955 ESIKEILNIYSSNIISL----LSENKPSYIEGLTILNKPTTSQEVLNNYFKVLNNSYIR 1009

Query: 260 DFWGNPLMYNKEYYMFN-----AGNKNSYIKLKKDSPVGEILTRSKY----NQ 303
 D L Y+K Y + N N N Y+ + + + L SK+ N
 Sbjct: 1010 DSNEERLEYHKTYQLDNYVFSDKPICEVKQNNNIYLTINNTNNLN--LQPSKFKLLSINS 1067

Query: 304 NSKYINYRDLYI-----GEKFI-IRRKSNSQSINDDIVRKEDYIYLDFFNLN 349
 N +Y+ D I EK+I I + Q I++ K+ I D F N

Sbjct: 1068 NKQYVQKFDEVIISILGNMEKYIDISEDNRLQLIDNKNGAKKMIISNDMFISN 1120

tr Q7WUH7 Botulinum neurotoxin type E (Fragment) [bont/E] 71 AA
Q7WUH7_CLOBU [Clostridium butyricum] align

Score = 49.3 bits (116), Expect = 2e-04
 Identities = 30/77 (38%), Positives = 44/77 (56%), Gaps = 7/77 (9%)

Query: 266 LMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKS 325
 L+Y+KEYY+ M N++T + DS T S N S + IY GK I+R +

Sbjct: 2 LLYDKEYYLLNLKPNNFINRRRTDS-----TLSINNIRSTILLANRLYSGIKVQIQRVN 55

Query: 326 NSQSINDDIVRKEDYIY 342
 NS S ND++VR +D++Y

Sbjct: 56 NS-STNDNLVRNDDHVY 71

tr Q8ILA2 Hypothetical protein [PF14_0343] [Plasmodium falciparum] 2269
Q8ILA2_PLAF7 (isolate 3D7) AA align

Score = 48.1 bits (113), Expect = 4e-04
 Identities = 89/379 (23%), Positives = 144/379 (37%), Gaps = 73/379 (19%)

Query: 25 EMFNKYNSEXXXXXXXXRYKDNNLIDLSGYGAKEVYDGVELNDKN----- 71
 E FNNK ++E +Y +N L+I+ Y K VY VE N+KN

Sbjct: 1373 EDFNKLDNEHSKD-----KYGENALINYV-YLNKGTVYKNVEKNEKNKKNKERTHVNTEI 1426

Query: 72 -----QFKLTSSANSKIRVTQNO---NIIFNSVFLDFSVFWIRIPKYKNDGIQNYIHN 122
 Q K +S +NSR + N ++ P L + + + + + + I

Sbjct: 1427 KLNIYQRKESSSDSNSENIDMNNLECTSLYFTKNDLQNKNLFDLLRNIDKKNLRDVIFK 1486

Query: 123 EYTIINCMKNNS---GWKISIRGNRIIWTLIDINGKTGSVFEYNIREDISEYINRWFFV 179
 + +IN + N G K + N I + K K+VF + + + Y NR

Sbjct: 1487 IFAVINSKRFNGDMIGEKGKFKNNEITKYI-----KNKNVFNKIKPYKKNTNYKNRK--- 1538

Query: 180 TITNNLNAKIYINGKLESNTDIKDIREVIANGEIIIFKLDGDIDRTQFIWMKYF----- 233
 N N K K E+ + K + + + I+ + + + K

Sbjct: 1539 --ENKKENKK---ENKKENKNNKKLHSFFIRNKLIYNNNNNSNNNNICKKNNNIQKISK 1593

Query: 234 -SIFNTELSQSNIIEERYKIQSYSEYLKDFWGNPLM---YNKEYYMFNAGNK-----N 281
 N +NI +R Q E K+ GN + YN +Y + N NK N

Sbjct: 1594 QKKINKIFYPTNIYKRM-YQKIKENNKNMEGNQKIIETYNTKYKLINVPNKEIYFHKNEN 1652

Query: 282 SYIKLKKDSPVGEILTRSKYNQNSKYI-----NYRDLYIGEKFIIRRKSNSQSINDDIVR 336
 + I +KK PV + R Q +KYY NY L+T +K ++ NS + N+ I+

Sbjct: 1653 NNIGVKKTLPV--YIYRMTMKQKNKYIPIKKFNYSYLFIEKK---KKNYSSTRNNKILP 1707

Query: 337 KEDYIYLDFFNLNQEWRVY 355
 + I+ Y N + + Y

Sbjct: 1708 YYYFFDLNNFTQNMQONLY 1726

Sbjct: 1068 NKQYYQKFDEVIISILGNMEKYIDISEDNRLQLIDNKNGAKKMIISNDMFISN 1120

tr Q7WUH7 Botulinum neurotoxin type E (Fragment) [bont/E] 71 AA
Q7WUH7_CLOBU [Clostridium butyricum] align

Score = 49.3 bits (116), Expect = 2e-04
 Identities = 30/77 (38%), Positives = 44/77 (56%), Gaps = 7/77 (9%)

Query: 266 LMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIIRRKS 325
 I+Y+KEYY+ N N++I + DS T S N S + LY G K I+R +

Sbjct: 2 LLYDKEYYLLNLKPNNFINRRRTDS-----TLSINNIRSTILLANRLYSGIKVVKIQRVN 55

Query: 326 NSQSINDDIVRKEDYIY 342
 NS S ND++VR +D++Y

Sbjct: 56 NS-STNDNLVRNDDHVY 71

tr Q8ILA2 Hypothetical protein [PF14_0343] [Plasmodium falciparum] 2269
Q8ILA2_PLAF7 (isolate AA
 3D7)] align

Score = 48.1 bits (113), Expect = 4e-04
 Identities = 89/379 (23%), Positives = 144/379 (37%), Gaps = 73/379 (19%)

Query: 25 EMFNKYNSEXXXXXXXXXRYKDNNLIDLSGYGAKEVYDGVELNDKN----- 71
 E FNK ++E +Y +N L+I+ Y K VY VE N+K+N

Sbjct: 1373 EDFNKLDNEHSKD-----KYGENALINYV-YLNKGTVYKNVEKNEKNKKNKERTHVNTEI 1426

Query: 72 -----QFKLTSSANSKIRVTQNQ---NIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHN 122
 Q K +S +NSK + N ++ F I + + + + + + + I

Sbjct: 1427 KLNIYQRKESSSDSNSENIDMNNLECTSLYFTKNDLQNKNLFDLLRNIDKKNLRDVIFK 1486

Query: 123 EYTIINCMKNNS---GWKISIRGNRIIWTLIDINGKTCSVFFEYNIREDISEYINRWFFV 179
 + +IN + N G K + N I + K K+VF + + + Y NR

Sbjct: 1487 IFAVINSKRFNGDMIGEKGFKNNEITKYI----KNKNVFNKIKPYKKNTNYKNRK--- 1538

Query: 180 TITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYF----- 233
 N N K K E+ + K + + + I+ + + + K

Sbjct: 1539 --ENKKENKK---ENKKENKKKLHSFFIRNKLIYNNNNNSNNNICKKNNIQKISK 1593

Query: 234 -SIFNTELSQSNIIEERYKIQSYSEYLKDFWGNPLM---YNKEYYMFNAGNK-----N 281
 N +N+I +P Q E K+ GN + YN +Y + N NK N

Sbjct: 1594 QKKINKIFYPTNIYKRM-YQKIKENNKNMEGNQKIIETYNTKYKLINVPNKEIYFHKNEN 1652

Query: 282 SYIKLKKDSPVGEILTRSKYNQNSKYI-----NYRDLYIGEKFIIIRRKSNSQSINDDIVR 336
 + I +NK PV + R Q +KYI NY L+I +K ++ NS + N+ I+

Sbjct: 1653 NNIGVKKTLPV--YIYRMTMKQKNKYIPIKKFNYSYLFIEKK---KKNYNSSTRNNKILP 1707

Query: 337 KEDYIYLDFFNLNQEWRVY 355
 + I+ F N + +Y

Sbjct: 1708 YYYFFDLNNFTQNMQONLY 1726

Score = 35.8 bits (81), Expect = 2.0
 Identities = 49/211 (23%), Positives = 89/211 (41%), Gaps = 19/211 (9%)

Query: 152 INGKTKSVFFEYNIRE---DISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKD-IR 206
 Sbjct: 815 ISDSEENIHYESNIKVNVNNSSEHLSDYCYDKNSSNYNNSEGYINNNVEKENDQYDEKR 874

Query: 207 EVIANGEIIFK-LDGIDIDRTQFIWMKYFSIFNTELSQSNIERYKI-----QSYSEYL 258
 Sbjct: 875 SIQYNGNSYDKSYSSYSDRAQKDIYGYKSICSEDNSKNMNSKDSIAIIKSITSANSEEK 934

Query: 259 KDF-WGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSK-YNQNSKYINYRDLYIG 316
 Sbjct: 935 KEMKYNKNIIYNNDCNDNDYVNSFYDLYDQEKFDEISQKNKIITRIGSFVTNKS VYQY 994

Query: 317 EKFIIRRKSNSQSINDDIVRKEDYIYLDFFN 347
 Sbjct: 995 EKY----KKDQSSTS VVIPSKYDTHFNDIEN 1021

tr Q8IBF4 Hypothetical protein MAL7P1.167 [MAL7P1.167] 2773
Q8IBF4_PLAF7 [Plasmodium falciparum AA
 (isolate 3D7)] align

Score = 47.8 bits (112), Expect = 5e-04
 Identities = 82/340 (24%), Positives = 129/340 (37%), Gaps = 35/340 (10%)

Query: 21 TILIEMFNKYNSEXXXXXXXXXRYKDNNLIDLGYAKVEVYDGVELNDKNQFKLT-SSA 79
 Sbjct: 44 TNLFKFNGKYENRIIHDDSTTSYTPNNAIEKNNNGN---CNRSNNNTQNYIKLLQSNV 99

Query: 80 NSKIRVTQNQNIIFNSVFLDFSVFWIRIPKYKNDGIQNYIHN---EYTIINC MKNNSG 135
 Sbjct: 100 NFNKIKTPQENTIINLNKINQLHN-----KNQICSRINNLNCNYDEQLCNILNNNEK 151

Query: 136 WKISIRGNRIIWTLIDINGKTKSVFFEYN--IREDISEYINRWFFVTITNNLNNAKIYIN 193
 Sbjct: 152 DKKKLHGNNNIITHNHQNNITSTLYNYDNSCIENNQSDYINK--LSIKNKVNTSNTFYN 208

Query: 194 ---GKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIERY 249
 Sbjct: 209 IDQFGLLNKKKKIKSLE---NLKSYISNDGESFNNSTIKPFNSYNKSTMVKVNLSNE 264

Query: 250 KIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYQNS-KYI 308
 Sbjct: 265 KTILCRKNCKN FILNKRI-NLEHYNSKKGNSNNDMNESDVVKNYKQDYGNNNNSNNYY 323

Query: 309 NYRDLYIGEKFIIIRRKSNSQSINDD-IVRKEDYIYLDFFN 347
 Sbjct: 324 YYSDNYINDDNNNNYNNYYYDDDDGDIKKGEHIY--FYN 361

tr Q7WRP2 Botulinum neurotoxin type E (Fragment) [bont/E] 71 AA
Q7WRP2_CLOBU [Clostridium butyricum] align

Score = 35.8 bits (81), Expect = 2.0
 Identities = 49/211 (23%), Positives = 89/211 (41%), Gaps = 19/211 (9%)

Query: 152 INGKTKSVFFEYNIRE---DISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKD-IR 206
 T+ +++ +E NI++ Y++ + + ++N NN++ YIN +E D S R
 Sbjct: 815 ISDSEENIHYESNIKVNNYSSEHYSYLDYCYDKNSSNYNNSEGYINNNVEKENDQYDEKR 874

Query: 207 EVIANGEIIIFK-LDGIDIDRTQFIWMKYFSIFNTELSQSNEERYKI-----QSYSEYL 258
 + NG K DR Q Y SI + + S++ + I + SE
 Sbjct: 875 SIQYNGNSYDKSYSSYSDRAQKDIYGYKSICSEDNSKNMNSKDSIAIKSITSANSEEK 934

Query: 259 KDF-WGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSK-YNQNSKYINYRDLYIG 316
 N+ + ++YN + N N NS+ L EI ++K + + + +Y
 Sbjct: 935 KEMKYNKNIIYNNDCNDCNDFNVNFYDLYDQEKFDEISQKNKIIIRIGSFVTNKSVDYQ 994

Query: 317 EKFIIRRKSNSQSINDDIVRKEDYIYIYLDFFN 347
 EK+ K + S + I E D + D N
 Sbjct: 995 EKY---KKDQSSTSVDVIPSVDTHFNDIEN 1021

tr Q8IBF4 Hypothetical protein MAL7P1.167 [MAL7P1.167] 2773
Q8IBF4_PLAF7 [Plasmodium falciparum AA
 (isolate 3D7)] align

Score = 47.8 bits (112), Expect = 5e-04
 Identities = 82/340 (24%), Positives = 129/340 (37%), Gaps = 35/340 (10%)

Query: 21 TILIEMFNKYNSEXXXXXXXXXRYKDNNLIDLSGYGAKVEVYDGVELNDKNQFKLT-SSA 79
 T L + KY + Y NN T+ + G + N + N KL S+
 Sbjct: 44 TNLFKFNGKYENRIIHDDSTTNSYTPNNAIEKNNNGN---CNRSNNNTQNYIKLLQSNV 99

Query: 80 NSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHN---EYTIINCMKNNSG 135
 N T +N I N ++ * KN N I+N + + N + NN
 Sbjct: 100 NFNKIKTPQENTIINLNKINQLHN-----KNQICSNRINNLNYDEQLCNILNNNEK 151

Query: 136 WKISIRGNRIIWTLIDINGKTKSVFFEYN--IREDISEYINRWFFVTITNNLNNAKIYIN 193
 K + GN I T N T + + N I + S+YIN+ + + I N +N + + N
 Sbjct: 152 DKKKLHGNNNIITHNHQNNITSTLYNYDNCIENNQSDYINK---LSIKNKVNNTSNTFYN 208

Query: 194 -----GKLESNTDIKDIREVIANGEIIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNEERY 249
 G I TK + N + DG+ F + S + + NE
 Sbjct: 209 IDQFGLLNKKKKIKSLE---NLKSYISNDGESFNNSFTIKPFNSYNKSTMVKVNLSNE 264

Query: 250 KIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNS-KYI 308
 K + K+F N + N E+Y GN M+ + D N NS Y
 Sbjct: 265 KTILCRKNCKNFIINKRI-NLEHYNSKKGNSNNDMNESDVVKNYKQDYGNNNNNNNYY 323

Query: 309 NYRDLYIGEKFIIIRRKSNSQSINDD-IVRKEDYIYIYLDFFN 347
 Y D YI + +N +DD + +K + +IY F+N
 Sbjct: 324 YYSDNYINDDNNNNYNNYYYDDDGDIKKGEHIY--FYN 361

tr Q7WRP2 Botulinum neurotoxin type E (Fragment) [bont/E] 71 AA
Q7WRP2_CLOBU [Clostridium butyricum] align

Score = 45.1 bits (105), Expect = 0.003
 Identities = 29/76 (38%), Positives = 42/76 (55%), Gaps = 7/76 (9%)

Query: 266 LMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKS 325
 L+Y+KEYY+ N N++I + DS T S N S + LY G R I+R +
 Sbjct: 2 LLYDKEYYLLNLKPNNFINRTDS-----TLSINNIRSTILLANRLYSGIKVKIQRVN 55

Query: 326 NSQSINDDIVRKEDYI 341
 NS S ND++VR +D +
 Sbjct: 56 NS-STNDNLVRNDDRV 70

tr Q6DN58 COX1 intron 3 ORF [COX1] [Kluyveromyces lactis (Yeast)] 396 AA
Q6DN58_KLULA
align

Score = 44.7 bits (104), Expect = 0.004
 Identities = 65/257 (25%), Positives = 105/257 (40%), Gaps = 47/257 (18%)

Query: 106 IRIPKYKNDGIQ-----NYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGTKS 158
 I+I KYK+ +Q N T+N +K+ I+I N +IW + UT
 Sbjct: 152 IQINKYKSKYLQFRLLIKLNNNKENINILNNIKHYLKGNIINNNYVIWIINDIK----- 206

Query: 159 VFFEYNIREDISEYINRWFFVTITNNLNNAKI----YI---NGKLESNTDIKDIREVIAN 211
 NI ++ + N++ +T+I L A I YI N I N +KD
 Sbjct: 207 -----NI-NNLIKLFNKYPLITINKKLQLAFIKEYIYKNNRNALINLYLKDRNN--KY 258

Query: 212 GEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIERYKI-QSYSEYLKDFWGNPLMYNK 270
 ++K DI+ T+ + YFS N + I I +Y+ + W + NK
 Sbjct: 259 NPPLYKYYKDINYTK---INYFSPANFHKKFAGININININNNYHNHYINVWFLGFIENK 315

Query: 271 EYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSI 330
 ++ N N++ D + E L ++ +N +K I +YI E + N I
 Sbjct: 316 GKFIIRKNNNNNSFLFYINDKHLIEFL-KNYFNKNIKLIYKNNIYILEVY-----NKYYI 368

Query: 331 NDDIVRKEDYIYLDFFN 347
 N I++ FEN
 Sbjct: 369 N-----IFIKEFN 376

tr Q8I5X3 Hypothetical protein [PFL0360c] [Plasmodium falciparum] 2723
Q8I5X3_PLAF7 (isolate 3D7)
AA
align

Score = 43.9 bits (102), Expect = 0.008
 Identities = 77/364 (21%), Positives = 136/364 (37%), Gaps = 61/364 (16%)

Query: 19 NDTILIEMFNKYNSEXXXXXXXXRYKDN--NLIDLGYGA-KVEVYDGVELNDKNQFKL 75
 N I I YN + D+ N + GY V + + N K
 Sbjct: 2276 NYDIFISQHKLYNDVTSMDKKEFNKQSDHIFNNYHIDGYNVDNRSSNHISNNNSIIINKR 2335

Query: 76 TSSANSKIRVTQ---NQNIIFNSVFLDFSWSWIRIPKYKNDGIQ-----NYIHN 122
 +N+K+ + N+N+TEN+ ++ + + + K N+ N +N
 Sbjct: 2336 QMMSNNKIVINNNHISNKNMIFNNNIINNNIIMYNK--KKSNNSSSCCINTMHGNNNNN 2393

Score = 45.1 bits (105), Expect = 0.003
 Identities = 29/76 (38%), Positives = 42/76 (55%), Gaps = 7/76 (9%)

Query: 266 LMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKS 325
 L+Y+KEYY+ N N++I + DS T S W S + LY G R T+R +
 Sbjct: 2 LLYDKEYYLLNVLKPNNFINRTDS-----TLSINNIRSTILLANRLYSGIKVKIQRVN 55

Query: 326 NSQSINDDIVRKEDYI 341
 NS S ND++VR +D +
 Sbjct: 56 NS-STNDNLVRNDDRV 70

tr Q6DN58 COX1 intron 3 ORF [COX1] [Kluyveromyces lactis (Yeast)] 396 AA
Q6DN58_KLULA
align

Score = 44.7 bits (104), Expect = 0.004
 Identities = 65/257 (25%), Positives = 105/257 (40%), Gaps = 47/257 (18%)

Query: 106 IRIPKYKNDGIQ-----NYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGTKS 158
 I+I KYK+ +Q N T+N +K+ I+I N +IW + UI
 Sbjct: 152 IQINKYKSKYLQFRLLIILNNNKENINILNNIKHYLGNININNNYVIWIINDIK---- 206

Query: 159 VFFEYNIREDISEYINRWFFVTITNNLNNAKI---YI---NGKLESNTDIKDIREVIAN 211
 NI ++ + N++ +TI L A I YI N L M +KD
 Sbjct: 207 -----NI-NNLIKLFNKYPLITINKKLQLAFIJKSIYYIYKNNRNALAINLYLKDRNN--KY 258

Query: 212 GEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSIEERYKI-QSYSEYLKDFWGNPLMYNK 270
 ++K DI+ T+ + YFS N + I I +Y+ + W + NK
 Sbjct: 259 NPPLYKYYKDINYTK---INYFSPANFHKKFAGININININNNYHNHYINVFLGFIENK 315

Query: 271 EYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSI 330
 ++ N NS++ D + E L ++ +N +K I ++YI E + N I
 Sbjct: 316 GKFIIRKNNNNNSFLFYINDKHLIEFL-KNYFNIKNLKLYKNNIYILEVY-----NKYYI 368

Query: 331 NDDIVRKEDYIYLDFFN 347
 N I++ FFN
 Sbjct: 369 N-----IFIKFFN 376

tr Q8I5X3 Hypothetical protein [PFL0360c] [Plasmodium falciparum] 2723
Q8I5X3_PLAF7 (isolate 3D7)
AA
align

Score = 43.9 bits (102), Expect = 0.008
 Identities = 77/364 (21%), Positives = 136/364 (37%), Gaps = 61/364 (16%)

Query: 19 NDTILIEMFNKYNSEXXXXXXXXRYKDN--NLIDLGYGA-KVEVYDGVELNDKNQFKL 75
 N I I YN + D+ N + GY V + + N K
 Sbjct: 2276 NYDIFISQHKLYNDVTSMDKKEFNQSDHIFNNYHIDGYNVDNRSSNHISNNNSIIINKR 2335

Query: 76 TSSANSKIRVTQ---NQNIIFNSVFLDFSVSFWIRIPKYKNDGIQ-----NYIHN 122
 +N+KI + N+N+TEN+ ++ ++ + + K N+ N +N
 Sbjct: 2336 QMMSNNKIVINNNHISNKNMIFNNNIINNNIIMYNK--KKSNNSSSCCINTMHGNNNNN 2393

Query: 123 EYTIINCMKNNSGWKISIRGNRIIWTLIDIN---GKTKSVFFEYNIREDISEYINRWFFV 179
 + N ++N + K I+ N I+ + N S F N E+ S + + V
 Sbjct: 2394 NFQCSNILRNMTNQKIDIKDNMILKKISTNNCEMNNLNCSFLSNSSENGSYKTDEFLNV 2453

Query: 180 TITNNLNNNAKIYINGKLESNTDIKDIREVIANGEIIIFKLDGDIDRTQFIWMKYFSIFNTE 239
 +N+ I + E N +K N +I DI+ + +
 Sbjct: 2454 NEKYRINDLNILHSNNKEVNNILKGHNIKHNNNKI----NDIN-----ILHSNN 2498

Query: 240 LSQSNIIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKN SYIKLK-----KDS 290
 +N+ I + + I+ + + D N L + E+Y + N S +K + +S
 Sbjct: 2499 KEVNNILKSHNIKHNNNKINDI--NILHSHNEFYNIHTNNHKSDLKCVGGHITNDRYENS 2556

Query: 291 PVGEILTRSKYN-----QNSKYI---NYRDLYIGEKFIIRRKSNSQSINDDIVR 336
 + #I T K N +N KY+ N+ ++Y+GE I+ N ND I +
 Sbjct: 2557 ILSQIKTHEKENIRQIKHTNIEEENKKYVLPVNHNIEYLGEHNKIKSDKNETQDNDTIGK 2616

Query: 337 KEDY 340
 K Y
 Sbjct: 2617 KIIY 2620

Score = 34.3 bits (77), Expect = 6.0
 Identities = 65/299 (21%), Positives = 120/299 (39%), Gaps = 36/299 (12%)

Query: 28 NKYNSEXXXXXXXXXRYKDNNLIDLSGYGAKVEVYDGVELNDKNQFKLTSSANSKIRVTQ 87
 N +NS RY +++ I + Y + Y + N+ + + +K +TQ
 Sbjct: 1271 NNHNSNNNNNHINRDRYINHHNIISNEYIRQQIKYTNINFNNHKND SINENVRNKSTITQ 1330

Query: 88 NQNIIFNS-----VFLDFSVFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKIS 139
 + +N+ D + I Y N+ + + +N + N NN+ +
 Sbjct: 1331 VNGLNYNTNEKDKEKINHNDNHIHTKRIIRNYSNNLDMHFMNNNIHLDDNNNNNNNNNN 1390

Query: 140 IRG-NRIIWTLI-----DINGKTKSVFFEYNIREDISEYINRWFFVTITNNLNNNAKIY-I 192
 N I W I K + F N +I ++ N + N +IY I
 Sbjct: 1391 NNNCNYIRWENIFFPYCNSCKNKYANKFEINNFDNNIMNKYEKYECTCCGNKIRNEEIYNI 1450

Query: 193 NGKLESNTDIKDIREV--IANGEIIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIIEERYK 250
 GK+ S + + + I + I N + I + + + WM F + +N E YK
 Sbjct: 1451 LGKVTS-E-NLRNIYKSNRINNTDNILRYNRENE-----WMSSFF----FKENNREIYK 1499

Query: 251 IQSYSEYLKDFWGNPLMYNKEYYMFNAGNKN SYIKLKKDSPVGEILTRSKYNQNSKYIN 309
 + Y EY DF+ N + E M N +N+ +K K + E +T++ N+ Y+N
 Sbjct: 1500 -EEYDEYKNDFFLN--IKEGEKSMLNNIFRNNSLKEKLINE--ENITKT---NNNVYVN 1550

tr Q7RP92 Clp [PY01567] [Plasmodium yoelii yoelii] 518 AA
Q7RP92_PLAYO align

Score = 43.5 bits (101), Expect = 0.010
 Identities = 65/268 (24%), Positives = 107/268 (39%), Gaps = 45/268 (16%)

Query: 100 FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSV 159
 FS+ + I K KN N IN +N + I S I N I++ K +
 Sbjct: 78 FSIKLLLIDKKVKNI-----NSLEKINMNENKIKYIISI--NLILFCY-----KII 121

Query: 160 FFNEYNIREDISEYINRWFFVTITNNLNNNAKIYINGKLESNTDIKDIREV----- 208

Query: 123 EYTIINCMKNNSGWKISIRGNRIIWTLIDIN---GKTKSVF FEYNIREDISEYINRWFFV 179
 + N ++N + KI I+ N I+ + N S F N E+ S + + V
 Sbjct: 2394 NFQCSNILRNMTNQKIDIKDNMILKKISTNNCEMNNLNCSFLSNSSSENGSYKTDEFLNV 2453

Query: 180 TITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIIFKLDGDIDRTQFIWMKYFSIFNTE 239
 +N+ I + E N +K N +I D+ + +
 Sbjct: 2454 NEKYRINDLNILHSNNKEVNNILKGHNKHNNNKI----NDIN-----ILHSNN 2498

Query: 240 LSQSNIIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKN SYIKLK-----KDS 290
 +N+ I + + T+ + + D N I + E+Y + N S +K + +S
 Sbjct: 2499 KEVNNILKSHNIKHNNNKINDI--NILHSHNEFYNIHTNNHKSDLKCVGGHITNDRYENS 2556

Query: 291 PVGEILTRSKYN-----QNSKYI---NYRDLYIGEKFII RRSNSQSINDDIVR 336
 + +I T K N +N KY+ N+ ++Y+GE I+ N ND I +
 Sbjct: 2557 ILSQIKTHEKENIRQIKHTNIEENKKYVLPVN HNEIYLGEHNKIKSDKNETQDNDTIGK 2616

Query: 337 KEDY 340
 K Y
 Sbjct: 2617 KIIY 2620

Score = 34.3 bits (77), Expect = 6.0
 Identities = 65/299 (21%), Positives = 120/299 (39%), Gaps = 36/299 (12%)

Query: 28 NKYNSEXXXXXXXXXRYKDNNLIDL SGY GAKVEVYDGVELNDKNQFKLTSSANSKIRVTQ 87
 N +NS RY + + + I + ? + Y + N + + + + +K +PQ
 Sbjct: 1271 NNHNSNNNNNHINRDRYINHHNIISNEYI RQQIKYTNINFNNHKNDSINENVRNKSTITQ 1330

Query: 88 NQNIIFNS-----VFLDFS VSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKIS 139
 + +N+ D + I Y N+ + + +N + N + NN+ +
 Sbjct: 1331 VNGLNYNTNEKDKEKINHNDNHIHTKRIIRNYSNNLDMHFMNNNIHLDNNNNNNNNNNNN 1390

Query: 140 IRG-NRIIWTLI-----DINGKTKSVF FEYNIREDISEYINRWFFVTITNNLNNAKIY-I 192
 N I W I K + F N +I ++ N + N +IY I
 Sbjct: 1391 NNNCNYIRWENIFFPYCNSCKNKYANKEINNFDNNIMNKYEKYECTCCGNKIRNEEYNI 1450

Query: 193 NGKLESNTDIKDIREV--IANGEIIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNI ERYK 250
 GK+ S + + + I + I N + I + + + WM F + + N E YK
 Sbjct: 1451 LGKV TSE-NLRNIYKSNRINTDNILRYNRENE-----WMSSFF-----FKENNREIYK 1499

Query: 251 IQSYSEYLKDFWGNPLMYNKEYYMFNAGNKN SYIKLKKDSPVGEILTRSKYNQNSKYIN 309
 + Y EY DE+ N + E MN +N+ +K K + E +P++ N+ Y+N
 Sbjct: 1500 -EEYDEYKNDFFLN--IKEGEKSM LNNI FRNNSLKEKLINE--ENITKT---NNNVYVN 1550

tr Q7RP92 Clp [PY01567] [Plasmodium yoelii yoelii] 518 AA
Q7RP92_PLAYO align

Score = 43.5 bits (101), Expect = 0.010
 Identities = 65/268 (24%), Positives = 107/268 (39%), Gaps = 45/268 (16%)

Query: 100 FSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSV 159
 FS+ + I K KN N I N +N + ISI N I++ E +
 Sbjct: 78 FSIKLLL DIKKVKNI-----NSLEKINMNENKIKYIISI--NLILFCY-----KII 121

Query: 160 FF EYNIREDISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREV----- 208

+ YN+ S +I R+ V+ NN IN + ++I ++

Sbjct: 122 KYIYNLFLSYSYFIFRFSVSNLNNKEFLLCIINNNIFLKKTENIYDIYLNKELNFY 181

Query: 209 IANGEIIFKLDGDIDRTQFIWMKYFSIF--NTELSQSNIER--YKIQSSEYLKDFWGN 264
 T EIIY++D DI + KY + F NTE+ +N++++ K+ + Y N

Sbjct: 182 IXQKEIIIFEMD-DIKKNSIFQKKYMNTFNTNTEIYPTNLDDKNINKVDNNMCYEDKVIKN 240

Query: 265 PLM---YNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFII 321
 + NKE Y N + N +K E L K ++ + N L KF+

Sbjct: 241 KIFEDATNKEKY--NKCDDNDSVKNNSSEYKDEFLINKKTHELDEKKNTLKSKNVKFL- 297

Query: 322 RRKSNSQSINDDIVRKEDYIYLDFFNLN 349
 +N + K ++Y+D F +N

Sbjct: 298 -----CVNKISIFKNMHLYIDKFYIN 318

tr Q7RDL0 Hypothetical protein [PY05412] [Plasmodium yoelii] 834
Q7RDL0_PLAYO yoelii AA
align

Score = 43.5 bits (101), Expect = 0.010
 Identities = 58/243 (23%), Positives = 108/243 (43%), Gaps = 36/243 (14%)

Query: 106 IRIPKYKNDGIQNYIHN-EYTIIN-----CMKNNSGWKISIRGNRIIWTLIDINGTK 157
 T+I KY+ D I I +Y++ N C KNN S +II +I + + K
 Sbjct: 283 IKIQKYEEDKIGEIICRLKYSLDNVNNGIEICKKNNFHMNFSELKEIIKSLNFFEHENK 342

Query: 158 SVFFEYNIREDISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFK 217
 +++PE D + + V + N++ ++IYI K + D+K + A I ++
 Sbjct: 343 NIYFEVIPTYDNLDLKGTEVVKV-KNIDISEIYI--KKNISNDLKLFFNKQAOQ-NIYYQ 398

Query: 218 LDGDIDRTQFIWMKYFSIFNTELSQSNIERYK-----IQSYSEYLKDFWGNPLMY 268
 +G++ + ++ K F + N + NI R I +Y++ +KD++ + Y
 Sbjct: 399 YNGELTQLYNLFEKNFIVLNDQFKIMNISNRKNISSLNNAIINTYNK-IKDYYKPAIYY 457

Query: 269 NKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQ 328
 N MA N + + +I+ + + N N++Y N + +K I N +
 Sbjct: 458 NN----LNALN-----NVETHLQDIIQIEANLNTENYKNNFEF---QKKFINVGINQE 503

Query: 329 SIN 331
 SIN
 Sbjct: 504 SIN 506

tr Q6LFF0 Hypothetical protein [PFF0575c] [Plasmodium falciparum] 3248
Q6LFF0_PLAF7 (isolate 3D7) AA
align

Score = 43.5 bits (101), Expect = 0.010
 Identities = 52/241 (21%), Positives = 99/241 (40%), Gaps = 35/241 (14%)

Query: 113 NDGIQNYIHNEYTII-----NCMKNNSGWKISIRGNRIIWTLIDINGTKSVFFEYNIR 166
 N I N + + N RI+ + + NN S N + + ++ + N+
 Sbjct: 1585 NQNIHNRMNNTNTIVQNNVRSSILLNNKNNNSSSNNNL PYDKENVTNIKYDLLNNKNVH 1644

+ YN+ S +I R+ V+ NN IN + ++I ++

Sbjct: 122 KYIYNLFLSYFIFRFSSVSNNKEFLLCIINNNIFLKKTENIYDIYLNKELFNFY 181

Query: 209 IANGEIIFKLDGDIDRTQFIWMKYFSIF--NTELSQSNIER--YKIQSSEYLKDFWGN 264
 T EIIY++D DI + KY + R NTE+ +N++++ E+ + Y N

Sbjct: 182 IXQKEIIIFEMD-DIKKNSIFQKKYMNTFNTNEIYPTNLDDKNINKVDNNMCYEDKVIKN 240

Query: 265 PLM---YNKEYYMFNAGNKNYSIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFII 321
 + NKE Y N + N +K E L K ++ + N L KF+

Sbjct: 241 KIFEDATNKEKY--NKCDDNDSVKNNSSEYKDEFLINKKTHELDEKKNTLKLSKNVKFL- 297

Query: 322 RRKSNSQSINDDIVRKEDYIYLDFFNLN 349
 +N + K ++Y+D F +N

Sbjct: 298 -----CVNKISIFKNMHLYIDKFYIN 318

tr Q7RDL0 Hypothetical protein [PY05412] [Plasmodium yoelii] 834
Q7RDL0_PLAYO yoelii
align

Score = 43.5 bits (101), Expect = 0.010
 Identities = 58/243 (23%), Positives = 108/243 (43%), Gaps = 36/243 (14%)

Query: 106 IRIPKYKNDGIQNYIHN-EYTIIN-----CMKNNSGWKISIRGNRIIWTLIDINGKTK 157
 T+I KY+ D I I +Y++ N C KNN S +II +I + + K
 Sbjct: 283 IKIQKYEEDKIGEICRLKYSLDNVNNGIEICKKNNFHMNFSELKEIIKSLNFFEHENK 342

Query: 158 SVFFEYNIREDISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFK 217
 +++FE D + + V + N++ ++IYI K + D+K + A I ++
 Sbjct: 343 NIYFEVIPTYDNLDLKGTEVVKV-KNIDISEIYI--KKNISNDLKLFFNQAO-NIYYQ 398

Query: 218 LDGDIDRTQFIWMKYFSIFNTELSQSNIERYK-----IQSYSEYLKDFWGNPLMY 268
 +G++ + ++ K F + N + NI R I +Y++ +KD++ + Y
 Sbjct: 399 YNGELTQLYNLFEKNFIVLNDQFKIMNISNRKNIISSLNNAIINTYNK-IKDYYKPAIYY 457

Query: 269 NKEYYMFNAGNKNYSIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQ 328
 N NA N + + + +I+ + + N N++Y N + +K I N +
 Sbjct: 458 NN----LNALN-----NVETHLQDIIIIQIEANLNTYEKNNFEF---QKKFINVGINQE 503

Query: 329 SIN 331
 SIN
 Sbjct: 504 SIN 506

tr Q6LFF0 Hypothetical protein [PFF0575c] [Plasmodium falciparum] 3248
Q6LFF0_PLAF7 (isolate 3D7)
align

Score = 43.5 bits (101), Expect = 0.010
 Identities = 52/241 (21%), Positives = 99/241 (40%), Gaps = 35/241 (14%)

Query: 113 NDGIQNYIHNNEYTII-----NCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIR 166
 N I N +N RT+ + + NN S N + + ++ + N+
 Sbjct: 1585 NQNIHNRMNNTNTIVQNNVRSSILLNNKNNNSSSNNNNLPYDKENVNTNIKYDLLNNKNVH 1644

Query: 167 EDISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDG----D 221
 +T F+ NNN+ + N + N +DI + NG+I+ +G +
 Sbjct: 1645 NNIP-----FIGTKINLNNSLVQLNNNMNKNILSEDINK---NGDILNSFNGNALPIN 1694

Query: 222 IDRTQFIWMKYFSIFNTELSQSNIIEERYKIQSYSEYLKD-FWGNPLMYNKEYYMFNAGNK 280
 DR ++ +S NP ++++ + ++ S +L F N + NX N+ N+
 Sbjct: 1695 YDRNEY--ASSYSEKNTNINETYMNSMINSKNNSIHLNQMFTKNTITSNK----NSSNE 1747

Query: 281 NSYIKLKKDSPVGEI--LTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKE 338
 + KK + I L + N N +IN +T ++R SR D + K+
 Sbjct: 1748 KQIMNRKKLTKTQNINNLKATDINSNINFIN---HINNNSDVKRMSNFNIHRDGMYLKD 1803

Query: 339 D 339
 +
 Sbjct: 1804 E 1804

tr Q8IDG1 Hypothetical protein PF13_0283 [PF13_0283] [Plasmodium 595
 Q8IDG1_PLAF7 falciparum AA
 (isolate 3D7)] align

Score = 43.1 bits (100), Expect = 0.013
 Identities = 42/170 (24%), Positives = 73/170 (42%), Gaps = 33/170 (19%)

Query: 186 NNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYF----- 233
 NN K YIN K N + DI+++ N I + +++ + KY+
 Sbjct: 112 NNNKCYINVKNSFNNEINDIKQMOKNSYINY----LNKLKKNGNKYYDTCQNNIYGKET 166

Query: 234 ---SIFNTELSQSNIIEERYKIQSYSEYL-----KDFWG--NPLMYNKEYYMFNAGNKS 282
 +T+ T +S S+ + + S+ +Y + +G N + YN + + N EN
 Sbjct: 167 QVDNIYRTNMSTSSKKYMMNNMNSFGKYTINNIKNNIYGTNNNINYNIQQFNINCNEKNC 226

Query: 283 YIKLKKDSPVGEILTRSKYNQNSKYINY--RDLYIGEKFIIRRKSNSQSI 330
 + KL K G I T S N + Y Y + + I K +T+K + I
 Sbjct: 227 FHKLNKS---GLIKTYSFNNYKNSYATYKQKQIIINKNSLIQKKGENNYI 273

tr Q8I3X5 Hypothetical protein PFE0655w [PFE0655w] [Plasmodium 2763
 Q8I3X5_PLAF7 falciparum AA
 (isolate 3D7)] align

Score = 43.1 bits (100), Expect = 0.013
 Identities = 69/338 (20%), Positives = 135/338 (39%), Gaps = 43/338 (12%)

Query: 12 FDLSIYTNDTILIEMFNKYNSEXXXXXXXXRYKDNNLIDLSGYGAKVEVYDGVELNDKN 71
 +D +IY IL++ ++N + +NN + Y + VY ++N
 Sbjct: 1744 YDENIYNGSYILLD---EHNFKEPTNKMNNNNNNKKNVYYNCLVVYPYIDIN--- 1797

Query: 72 QFKLTSSANSKIRVTQN--QNIIFNSVFLDFSVSFW-----IRIPKYKNDGIQNYIHNE 123
 K+T++ + V++ + I N+ ++++ + F + I + +Q HN
 Sbjct: 1798 --KITTNISSDKNVSKELFEKDIMNNYYINYPILFLSNYKGKLYIHPLNKEKLQQSYHNN 1855

Query: 124 YTIIINCMKNNSGWKISIRGNRIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITN 183
 KNN+ + I N I++ + DI G N + + E IS N++
 Sbjct: 1856 KEEKEPNKNNNNYIIHYAHNNILYNIKDIYGHIKGL-HKIDQNEFISFSNNKFQIF--- 1910

Query: 167 EDISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDG----D 221
 +T F+ NLNN+ + N + N +DI + NG+I+ +G +
 Sbjct: 1645 NNIP-----FIGTKINLNNSLVQLNNNMNKNILSEDINK---NGDILNSFNGNALPIN 1694

Query: 222 IDRTQFIWMKYFSIFNTELSQSNIIEERYKIQSYSEYLKD-FWGNPLMYNKEYYMFNAGNK 280
 DR ++ +S NR ++++ + + +S +L F N + NK N+ N+
 Sbjct: 1695 YDRNEY--ASSYSEKNTNINETYMNSMINSKNNSIHLNQMFTKNTITSNK----NSSNE 1747

Query: 281 NSYIKLKKDSPVGEI--LTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKE 338
 + KK + I L + NN +IN +T ++R SN D + K+
 Sbjct: 1748 KQIMNRKKLTKTQNINNLKATDINSNINFIN---HINNNSDVKRMSNFNIHRDGMYLKD 1803

Query: 339 D 339
 +
 Sbjct: 1804 E 1804

tr Q8IDG1 Hypothetical protein PF13_0283 [PF13_0283] [Plasmodium 595
 Q8IDG1_PLAF7 falciparum AA
 (isolate 3D7)] align

Score = 43.1 bits (100), Expect = 0.013
 Identities = 42/170 (24%), Positives = 73/170 (42%), Gaps = 33/170 (19%)

Query: 186 NNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYF----- 233
 NN K YIN K N + DI+++ N I + +++ + EY+
 Sbjct: 112 NNNKCYINVKNSFNNERNDIKQMOKNSYINY----LNKLKKNGNKYYDTCONNIGKET 166

Query: 234 ---SIFNTELSQSNIIEERYKIQSYSEYL-----KDFWG--NPLMYNKEYYMFNAGNKNS 282
 +I+ T +S S+ + + S+ +Y + +G N + YN + + N KN
 Sbjct: 167 QVDNIYRTNMSTSSKKYMMNNMNSFGKYTIINNIKNNIYGTNNNINYNQQFNINCNEKNC 226

Query: 283 YIKLKKDSPVGEILTRSKYNQNSKYINY--RDLYIGEKFIIRRKSNSQSI 330
 + KL K G I T S N + Y Y + + I K +I+K + T
 Sbjct: 227 FHKLNKS---GLIKTYSFNNYKNSYATYKQKQIIINKSLIQKKGENNYI 273

tr Q8I3X5 Hypothetical protein PFE0655w [PFE0655w] [Plasmodium 2763
 Q8I3X5_PLAF7 falciparum AA
 (isolate 3D7)] align

Score = 43.1 bits (100), Expect = 0.013
 Identities = 69/338 (20%), Positives = 135/338 (39%), Gaps = 43/338 (12%)

Query: 12 FDLSIYTNDTILEMFNKNSEXXXXXXXXXXRYKDNNLIDLSGYGAKVEVYDGVELNDKN 71
 +D +IY IL++ +N + +NN + Y + VY + +N
 Sbjct: 1744 YDENIYNGSYILLD---EHNFKEPTNKMNKKNNNNNNKKNVYYNCLVVYPYIDIN--- 1797

Query: 72 QFKLTSSANSKIRVTQN--QNIIFNSVFLDFSVSFW-----IRIPKYKNDGIQNYIHNE 123
 K+T++ + V++ + I N+ +++++ + F + I + +Q HN
 Sbjct: 1798 --KITTNISSDKNVSKELFEKDIMNNYYINYPILFLSNYKGKLYIHPLNKEKLQQSYHNN 1855

Query: 124 YTIIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITN 183
 KN+ + I N I++ + DI G K + + E IS N++
 Sbjct: 1856 KEEKEPNKNNNNYIIHYAHNNILYNIKDIYGHIGL-HKIDQNEFISFSNNKFQIF---- 1910

Query: 184 NLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQS 243
 N+N+ K N + +T + + II + + + N + +
 Sbjct: 1911 NINDYK--YNSVMPKSTQVNIRSDFFLTSTIINEQSNESNN-----NNNNNNN 1956

Query: 244 NIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKN SYIKLKKDSPVGEILTRSKYNQ 303
 N I + K+ +GN + N Y + G+ NSY S +I+ SK
 Sbjct: 1957 NNNNNNNINNNNGN--KNNYGNKIHLLNPYGDTHIGHINSYSNPNHISIQNDIIFFSK--- 2011

Query: 304 NSKYINYRDLYIGEKFII RKSNSQSINDDIVRKEDYI 341
 NS IN L + E ++ + T+ + K+DX+
 Sbjct: 2012 NSNLIN---LSFNDSFATKKILSYPYIHKMCISKDDYV 2046

tr Q7RJM7 Hypothetical protein [PY03232] [Plasmodium yoelii] 1652
Q7RJM7_PLAYO yoelii] AA
align

Score = 43.1 bits (100), Expect = 0.013
 Identities = 64/305 (20%), Positives = 108/305 (34%), Gaps = 59/305 (19%)

Query: 14 LSIYTNDT---ILIEMFNKYNSEX XXXXXXXXRYKDNNLIDL SGYGA KVEVYD--GVEL 67
 LS Y +D I+ Y S Y +NN+ +D S + +D +
 Sbjct: 328 LSFYCDDDDDNKII FPPRQNYQSSTLQKL TGMLNYNNNIVDKSALDRSMSYFDLRREKK 387

Query: 68 ND--KNQFKLTSSANSKIRVTQNQNIIFNSVF LDFS VSFWIRIPKYKNDGIQNYIHNEYT 125
 ND KN K+ M IR N++ N++ NYIH +
 Sbjct: 388 NDIVKNYIKINKVRNGNIR---NEDNATNNIF-----NNYIHKD-- 423

Query: 126 IINC MKNNSGWKISIRGNRIIWTLDINGKTKSVFF EYNIRE DISEYINRWFFVTITNNL 185
 KT + G L + + + + +YN D I R + I N +
 Sbjct: 424 -----ENRKIYVHGEN---DLNNVDMHRNAFDHDYNK NYDTMHNIRRSTNI-IDNLV 471

Query: 186 NNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNI 245
 +N +Y N + +N + +I I N + ++ LD E NT N
 Sbjct: 472 HNRLVYNNNHFNNNENINILNKITNPDTVYPLD-----FRSNNT HDGICNN 518

Query: 246 EERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKN SYIKLKKDSPVGEILTRSKYNQNS 305
 +Y Y+ + N +Y+K +M N ++ +K E+L +
 Sbjct: 519 IGYK--DRYNNFNYKTIDNKYIYDKNNFMHENENYVNF SYIKNIEKF KELLINIATDNLK 576

Query: 306 KYINY 310
 +Y+ Y
 Sbjct: 577 EYVKY 581

tr Q9EMF0 AMV256 [AMV256] [Amsacta moorei entomopoxvirus (AmEPV)] 609 AA
Q9EMF0_AMEPV
align

Score = 42.4 bits (98), Expect = 0.022
 Identities = 87/373 (23%), Positives = 148/373 (39%), Gaps = 83/373 (22%)

Query: 17 YTNDTILIE MFN-KYNSEX XXXXXXXXRYKDNNLIDL SGYGA--KVEVYDGVELNDKNQF 73
 Y N +LT + + K S YK N + Y K+E D V LN+ E

Query: 184 NLNNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGIDRTQFIWMKYFSIFNTELSQS 243
 N+N+ K N + +T+ + + II + + + N + +
 Sbjct: 1911 NINDYK--YNSVMPKSTQVNIRSDFFLTSTIINEQSNESNN-----NNNNNNN 1956

Query: 244 NIEERYKIQSSEYLKDWFGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQ 303
 N T + K+ +GN+ N Y + G+ NSY S +I+ SK
 Sbjct: 1957 NNNNNNNINNNNGN--KNNYGNKIHLLNPYGDTHIGHINSYSNPNHISIQNDIIFFSK--- 2011

Query: 304 NSKYINYRDLYIGEKFIIIRRKSNSQSINDDIVRKEDYI 341
 NS IN L + F ++ + T+ + K+DX+
 Sbjct: 2012 NSNLIN---LSFNDSFATKKILSYPIHKMCISKDDYV 2046

tr Q7RJM7 Hypothetical protein [PY03232] [Plasmodium yoelii] 1652
Q7RJM7_PLAYO yoelii] AA
align

Score = 43.1 bits (100), Expect = 0.013
 Identities = 64/305 (20%), Positives = 108/305 (34%), Gaps = 59/305 (19%)

Query: 14 LSIYTNDT---ILIEMFNKYNSEXXXXXXXXRYKDNNLIDLGSYGAKEVEVD--GVEL 67
 LS Y +D I+ Y S . Y +NN+ +D S + +D +
 Sbjct: 328 LSFYCDDDDDNKIIFFPRQNYQSSTLQKLTMGLNYNNNIVDKSALDRSMSYFDLRREKK 387

Query: 68 ND--KNQFKLTSSANSKIRVTQNQNIIFNSVFVLDGSVSFWIRIPKYKNDGIQNYIHNEYT 125
 ND KN K+ M TR N++ N++ NYI+ +
 Sbjct: 388 NDIVKNYIKINKVRNGNIR---NEDNATNNIF-----NNYIHKD-- 423

Query: 126 IINC MKNNSGWKISIRGNRIIWTLDINGTKSVFFEYNIREDISEYINRWFFVTITNNL 185
 KT + G L +++ + +YN D I R + I N +
 Sbjct: 424 -----ENRKIYVHGEN---DLNNVDMHRNAFDHDYNKNYDTMHNIRRSTNI-IDNLV 471

Query: 186 NNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGIDRTQFIWMKYFSIFNTELSQSNI 245
 +N +Y N + +N + +I T N + ++ LD F NT N
 Sbjct: 472 HNRLVYNNNHFNNNENINILNKITNPDTVYPLD-----FRSNNTHDGICNN 518

Query: 246 EERYKIQSSEYLKDWFGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNS 305
 +Y Y+ + N +Y+K +M N ++ +K E+L +
 Sbjct: 519 IGKY--DRYNNFNYKTIDNKYIYDKNNFMHENENYVNFSYIKNIEKFELLINIATDNLK 576

Query: 306 KYINY 310
 +Y+ Y
 Sbjct: 577 EYVKY 581

tr Q9EMF0 AMV256 [AMV256] [Amsacta moorei entomopoxvirus (AmEPV)] 609 AA
Q9EMF0_AMEPV
align

Score = 42.4 bits (98), Expect = 0.022
 Identities = 87/373 (23%), Positives = 148/373 (39%), Gaps = 83/373 (22%)

Query: 17 YTNDTILIEMFN-KYNSEXXXXXXXXRYKDNNLIDLGSYGA--KVEVYDGVELNDKNQF 73
 Y N +I+ + + K S YK N + Y K+E D V LN+ F

Sbjct: 255 YYNKLVLINILSDKLLSLTIYFLTSEYMYKSLNYFETIDYSKIKKLEFDDYVILNE--YF 312
Query: 74 KLTSSANSKIRVTQNQNIIFNSVFLDFSVS-----FWIRIPKYKNDGIQNYIHNEYTI 126
+ + N+ + N+ + + +DT+ ++ F+++TP Q Y++NET+ I
Sbjct: 313 DIINIYNNNIKSNNINKYYSYNNKYIDYIINSSTDINKFFLQIPN-----QLYLNNEFDI 366
Query: 127 INCMKNNSGWKISIRGNRIIWTLIIDINGKTGSVFFEYNIREDISEYINRWFFVTITN-NL 185
N + + + I+ N K N NT + I N N+
Sbjct: 367 NNIPV-----FKAETLFNSKINTNNKNKIT---NINN-----IEILNFNV 403
Query: 186 NNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQ-----FIWMKYFSIFN 237
NN + + N + E + I K + + I N + I + K D + I + + KYF I+
Sbjct: 404 NNMIFFMN-VIEDKFEIKNNEIIIKNTKNIYKSDNNICVLNNNNYNPKIYFYYKYFIIYF 462
Query: 238 TELSQSNIEERYKIQSYSEYL-----KDFWGNPLMYNKE-----YYMFN 276
NT++ + Y Y + E N L+ NK+ Y++N
Sbjct: 463 FSNIFLNNIDDAIEYVKYKPYFNLLNNINVENNFTNLINNNKKININTNHDFITALYIYN 522
Query: 277 AGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVR 336
NKN YI + + + + IL R + IN+ + + FTE K+ I+ + R
Sbjct: 523 CNNKNCYIHM---ATISDIL-RDLGLIYTPIINFENNLV-YLFIITNKPHETEIH---LR 574
Query: 337 KEDYIYLDFFNLN 349
K I D FN+N
Sbjct: 575 K---ILNDKFNVN 584

tr Q8IIK5 Hypothetical protein [PF11_0168] [Plasmodium falciparum] 2966
Q8IIK5_PLAF7 (isolate AA
3D7)] align

Score = 42.0 bits (97), Expect = 0.029
Identities = 91/406 (22%), Positives = 160/406 (38%), Gaps = 76/406 (18%)

Query: 44 YKDNNLIDLSGYAKVEVYDGVELNDKNQFK---LTSSANSK-----RVTQNQNIIFNS 95
Y+----N + + + K +Y+ NDK+ +K L S++ + K+ ++ +N+N+I +
Sbjct: 1342 YONSNCNSNKNSFNNKDHIYNNTMNNDKDTYKYGTLSNSDHKMNICDEKIKKKNNMINDI 1401

Query: 96 VFLDFSVFWIRIPKYKNDGQNY-IHNEYTIINCMKNNSGWKISIRG----NRIIWTL 149
+ + I N I NY I + T N N+ KE + N I T
Sbjct: 1402 NIONITDKHVI----NKNIINYKINENKTENNIPVNNKKNKILVNNNIHTYNNIHMTN 1455

Query: 150 IDINGKTKSVFFEYNIREDI-----SEYINRWFFVTITNNLNNAKIYINGKLESNT--D 201
I+ + K+ F EY B+ S+ IN T+ KNL K K+E+N
Sbjct: 1456 INALHEKKTKFGEYKYFEKLFFDCLKSKIINE--IKTLDDNNLKKKK--KKKKIETNKLES 1511

Query: 202 IKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIERYKIQ----- 252
X++ +T N ++ + + + S ++ + +N+ + + X
Sbjct: 1512 IONTINIILKNYSFLYPSKNNNNEOKKKKNSOSSTESSGTTNNNTDSKNDIHMNKKIEDTS 1571

Query: 253 ---SYSEYLKDWFGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYI 308
+YS K+ WG + FN K+ KD+ V + N N K +
Sbjct: 1572 HVMPNYSVGEKNSWKGKEKLKLMIDIYFNE-----KVLKDTNVSNNMNECISNGNIKOM 1624

Query: 309 NYRDLYIGEKFIIIRRKSNSQ-SINDDI--VRKEDYIYLDFFNLNQEWRVYXXXXXXXXX 364
+ + T EN N +MD+T * + # Y* E + E Y

Sbjct: 255 YYNKLVLINILSDKLLSLTIYFLTSEYMYKSLNYFETIDYSKIKKLEFDDYVILNE--YF 312

Query: 74 KLTSSANSKIRVTQNQNIIFNSVFLDFSVS-----FWIRIPKYKNDGIQNYIHNEYTI 126
+ + N+ N+ + + +D+ ++ F+++TF Q Y++NE+ I

Sbjct: 313 DIINIYNNIKSNINNKYYSYNNKYIDYIINSSTDINKFFLQIPN-----QLYLNNEFDI 366

Query: 127 INCMKNNSGWKISIRGNRIIWTLIDINGTKSVFFEYNIREDISEYINRWFFVTITN-NL 185
N + + + I+ N K K NI + I N N+

Sbjct: 367 NNIPV-----FKAETLFNSKINTNNKNKIT---NINN-----IEILNFNV 403

Query: 186 NNAKIYINGKLESNTDIKDIREVIANGEIIFKLDG DIDRTQ-----FIWMKYFSIFN 237
NN + + N + E + I+ N + T+K D + T + + KYF I+

Sbjct: 404 NNMIFFMN-VIEDKFEIKNNEIIKNTKNIYKSDNNICVLNNNNYNPKIYFYYKYFIIYF 462

Query: 238 TELSQS NIEERYKIQSYSEYL-----KDFWGNPLMYNKE-----YYMFN 276
NI++ + Y Y + F N L+ NK+ Y++N

Sbjct: 463 FSNIFLNIDDAIEYVKYKPYFNLLNNINVENNFNTNILINNNKININTNHDFITALIYIYN 522

Query: 277 AGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVR 336
NKN YI + + + IL R + IN+ + + FTE K + I+ + R

Sbjct: 523 CNNKNCYIHM--ATISDIL-RDLGLIYTPIINFENNLV-YLFIITNKPHETEIH--LR 574

Query: 337 KEDYIYLDFFNLN 349
K I D FN+N

Sbjct: 575 K---ILNDKFNVN 584

tr	<u>Q8IIK5</u>	Hypothetical protein [PF11_0168] [Plasmodium falciparum	2966
	Q8IIK5_PLAF7	(isolate	AA
		3D7)]	<u>align</u>

Score = 42.0 bits (97), Expect = 0.029
 Identities = 91/406 (22%), Positives = 160/406 (38%), Gaps = 76/406 (18%)

Query: 44 YKDNNLIDLGYGAKVEVYDGVELNDKNQFK---LTSSANSKI----RVTQNQNIIFNS 95
Y+++N + + + K +Y+ NDK+ +K L S+++ N+ ++ +N+N+I +
Sbjct: 1342 YQNSNCNSKNSFNNKDHINYNTMNNDKTYKGTLNSNSDHKMNICDEKIKKNKNMINDI 1401

Query: 96 VFLDFSVSFWIRIPKYKNDGIQNY-IHNEYTIINCMKNNSGWKISIRG----NRIIWTL 149
+ + I N I NY I+ T N N+ KI + N I T
Sbjct: 1402 NIQNITDKHVI-----NKNIINYKINENKTENNIPLVNNKPKILVNNNIHTYNNIHMTN 1455

Query: 150 IDINGKTKSVFFEYNIREDI-----SEYINRWFFVTITNNLNNNAKIYINGKLESNT--D 201
I+ + K+ F EY S+ IN T+ NNL K K+E+N
Sbjct: 1456 INALHEKKTKFGEYKYFEKLFDFCLKSKIINE--IKTLDNNLKKKK--KKKIKETNKLFS 1511

Query: 202 IKDIREVIANGEIIFKLDG DIDRTQFIWMKYFSIFNTESQS NIEERYKIQ----- 252
I++ + I N + + + + S + + + +N+ + I
Sbjct: 1512 IQNTINIICKNYSFLYPSKNNNNEQKKKKNSQSSTESSGTTNNNIDSKNDIHMNKKLEDTS 1571

Query: 253 ----SYSEYLKDFWGNPLMYNKEYYMFnAGNKNsyIKLKKDSPVGEILTRSKYNQNSKYI 308
+YS K+ WG + FN K+ KD+ V + N N K +
Sbjct: 1572 HVMPNYSVGEKNSWGKEKLKKLMDIYFNE-----KVLKDTNVSNMNECISNGNIQM 1624

Query: 309 NYRDLYIGEKFIIRRKSNSQ-SINDDI---VRKEDYIYLDFFNLNQEWRVYXXXXXXXXX 364
+ + I EK N +IND+I + + + Y+ F + E Y

Sbjct: 1625 DNQQEKINEKINESENVNENVNINDNINDNINEHEQTYIPFDDDQNEEYDYI----- 1676
 Query: 365 XXXXXAPISDSDEFYNTIQIKEYDEQPTYSC-QLLFKKDEE-STDE 408
 S+ FY+T + + + SC Q KKD+ TDE
 Sbjct: 1677 -----SEFFYSTSEENDMNPNNNLSCQHELKKDKNYITDE 1712

tr Q7RB20 Hypothetical protein [PY06328] [Plasmodium yoelii] 2746
Q7RB20_PLAYO yoelii] AA
align

Score = 42.0 bits (97), Expect = 0.029
 Identities = 63/306 (20%), Positives = 123/306 (39%), Gaps = 41/306 (13%)

Query: 19 NDTILIEMFN--KYNSEXXXXXXXXRYKDNNLIDLSSG-YGAKVEV---YDGVELNDKNQ 72
 NDT + E+ N YN+ + D+ ++ Y + + D + +N+ +
 Sbjct: 39 NDTYVNELNNTSNYNNNNNSNNNCDKSSDDLNLNIDPCYTNSININSNMDNINMNEDSN 98

Query: 73 FKLTSSANSKIRVTQNQNIIFNSVFL---DFSWSWIRIPKYKN---DGIQNYIHNEYTI 126
 + N+ + P N N+ ++ DF I.+ Y+N G N +Y +
 Sbjct: 99 ----ENMNTYVNTTMNHNVNSSTDHRNDDFKFHMKINLSAYRNIYEKGKGNAQPKKYNL 154

Query: 127 INC MKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNNLN 186
 + K + G ++ DIN + K RED +N +F+ ++ N+
 Sbjct: 155 -SVQKGSKGILLNTYNYFYNNFGDINKRNKK-----REDD---VNIYFYKKVSRNVP 203

Query: 187 NAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMK-YFSIFNTELSQSNI 245
 N Y N ++TD ++ + + + + QF + Y +F EL +NI
 Sbjct: 204 NC--YENESNQNDTDDDNVEKSNLNSKNYNYN----KQFFGINSYDKVFLKELKITNI 256

Query: 246 EERYKIQSSEYLKDFWGNPLMYNKEYYMFNAGNKNSYI---KLKKDSPVGELTRSKY 301
 + +YK +S +Y F P Y+ ++ + +YI +K +SP+ Y
 Sbjct: 257 DNKYKKKSVKKYNIPF--EPNFYSNRFFSDKNINENYIGNSKNVKVNSPLSVNNNIESY 314

Query: 302 NQNSKY 307
 N + Y
 Sbjct: 315 NDSEHY 320

tr Q8T186 Hypothetical protein [Dictyostelium discoideum (Slime mold)] 793
Q8T186_DICDI AA
align

Score = 41.6 bits (96), Expect = 0.037
 Identities = 50/183 (27%), Positives = 83/183 (45%), Gaps = 37/183 (20%)

Query: 55 YGAKVEVYDGVELNDKNQFKLTSSA---NSKIRVTQ---NQNIIFNSVFLDFSVFWI 106
 YG + VYU ++N + F + + A N+ I V N N I FN F + ++S
 Sbjct: 85 YG-QYSVYDSMDIN-RGSFIMENGAILNVNNSIYVKYYFEINSNSIFNPTFKNTTIS--- 139

Query: 107 RIPKYKNDGIQNYIHNEYTIINCMK---NNSGWKISIRGNRIIWTLIDING---KTKSV 159
 + G N +NC K NN+G I++ N + I++NG K NS
 Sbjct: 140 -TKNFIIGGFLNIYQKSNLFLNCNKLEINNNG-SINVENN---SKINLNGGLIMKDKSQ 193

Query: 160 FFNEYNIREDISE---YINRWFFVTITNNLNNAKIYINGKLESNTD---IKDIREVIANG 212

Sbjct: 1625 DNQQEKINEKINESENVNENVNINDNINDNINEHEQTYIPFDDDQNEEYDYI----- 1676
 Query: 365 XXXXXAPISDSDEFYNTIQIKEYDEQPTYSC-QLFKKDEE-STDE 408
 Sbjct: 1677 -----SEFYSTSEENDMNPNNNLSCQHELKKDKNYITDE 1712

tr Q7RB20 Hypothetical protein [PY06328] [Plasmodium yoelii] 2746
Q7RB20_PLAYO yoelii] AA
align

Score = 42.0 bits (97), Expect = 0.029
 Identities = 63/306 (20%), Positives = 123/306 (39%), Gaps = 41/306 (13%)

Query: 19 NDTILIEMFN--KYNSEXXXXXXXXRYKDNNLIDLSSG-YGAKVEV---YDGVELNDKNQ 72
 Sbjct: 39 NDTYVNELNNTSNYNNNNNSNNNCDKSSDDLNLNIDPCYTNSININSNMDNINMNEDSN 98

Query: 73 FKLTSSANSKIRVTQNQNIIFNSVFL---DFSVSFWRIPKYKN---DGIQNYIHNEYTI 126
 Sbjct: 99 ----ENMNTYVNTTMNHNVNSSTDSHRNDDFKFHMKINLSAYRNIYEKGKGNAQPKKYNL 154

Query: 127 INC MKNNSGWKISIRGNRIIWTLIDINGKTKSVFFFEYNIREDISEYINRWFFVTITNNLN 186
 Sbjct: 155 -SVQKGSKGILLNTYNYFYNNFGDINKRNKK-----REDD---VNIYFYKKVSRNVP 203

Query: 187 NAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMK-YFSIFNTELSQSNI 245
 Sbjct: 204 NC--YENESQNQNTDDDNVEKSNL DNSKNYNYN----KQFFGINSYDKVFLKELKITNI 256

Query: 246 EERYKIQSSEYLKDFWGNPLMYNKEYYMFNAGNKNSYI---KLKKDSPVGELTRSKY 301
 Sbjct: 257 DNKYKKKSVKKYNI PF--EPNFYSNRFFSDKNINENYIGNSKNVKVNSPLSVNNNIESY 314

Query: 302 NQNSKY 307
 Sbjct: 315 NDSEHY 320

tr Q8T186 Hypothetical protein [Dictyostelium discoideum (Slime 793
Q8T186_DICDI mold)] AA
align

Score = 41.6 bits (96), Expect = 0.037
 Identities = 50/183 (27%), Positives = 83/183 (45%), Gaps = 37/183 (20%)

Query: 55 YGAKVEVYDGVELNDKNQFKLTSSA---NSKIRVTQ---NQNIIFNSVFLDFSFWI 106
 Sbjct: 85 YG-QYSVYDSMDIN-RGSFIMENGAILNVNNSIYVKYYFEINSNSIFNPTFKNTTIS--- 139

Query: 107 RIPKYKNDGQNYIHNEYTIINCMK---NNSGWKISIRGNRIIWTLIDING---KTKSV 159
 Sbjct: 140 -TKNFIIGGFLNIYQKSNLFLNCNKLEINNNG-SINVENN---SKINLNGGLIMKDKSQ 193

Query: 160 FFNEYNIREDISE---YINRWFFVTITNNLNNAKIYINGKLESNTD---IKDIREVIANG 212

+ N +I+ +N+ F N +NN ++T+G L N D + D E+ NG
 Sbjct: 194 IYLNNNSNIEINGDAMLMNQSIF----NTMNNLDFISGSLHLNDDSLFLLFDNNEMTING 249

Query: 213 EII 215
 +++
 Sbjct: 250 DLL 252

tr Q7RTC2	Hypothetical protein (Fragment) [PY00072] [Plasmodium	3663
Q7RTC2_PLAYO	yoelii	AA
	yoelii]	<u>align</u>

Score = 41.6 bits (96), Expect = 0.037
 Identities = 66/310 (21%), Positives = 125/310 (40%), Gaps = 77/310 (24%)

Query: 45 KDNNLIDLSGYGAKVEVYDGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSF 104
 KDN ++ + ++ EV +GV++ N+F N +I N+ F+
 Sbjct: 6 KDNEVVICNEVVSEEVNVGVKVVSNNEF-----IDNNEVINNNEFI----- 47

Query: 105 WIRIPKYKNDGIQN-YIHNEYTIINCMKNNSGWKISIR---GNRII---WTL---IDIN 153
 Y N + N Y N+ N +N G+ S GN ++ W + +D N
 Sbjct: 48 -----YNNGVVGNFYSENKVVARDNGFVSNIGFGNSNGFNIGNNDVVGSGSWCVDNEVDNN 101

Query: 154 GKTKSV-FFEYNIREDISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANG 212
 K + F YN +E +N FV NN IY D++D + N
 Sbjct: 102 NKVVNYNGFIYNNEVYNNEIVNNNEFVN-----NNGFIY-----NDVRD--HEVVNN 146

Query: 213 EIIFKLDGDIDRTQFIWMKYFSIFNTELSQSIEERYKIQSYSEYLKDFWGNPLMYNKEY 272
 +++F D + , F I+N E+ +N+ + E +D N YN E
 Sbjct: 147 DVVFYNDDEVVRDNGF-----IYNNEVNNNNV-----VFYNDIIVRD---NGFFYND 191

Query: 273 YMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSIND 332
 N N + + E+++ S++ N++ +N ++Y GE +N++++ +
 Sbjct: 192 -----NNNEVNNNEVSDNEVSDSEIFIYNNNEVNNNEVYNGEVV-----NNNEAVQN 240

Query: 333 DIVRKEDYIY 342
 +++ +Y
 Sbjct: 241 GVIKNYGLMY 250

Score = 36.2 bits (82), Expect = 1.6
 Identities = 44/198 (22%), Positives = 73/198 (36%), Gaps = 38/198 (19%)

Query: 179 VTITNNLNNAKIYING-KLESNTDIKDIREVIANGEIIF-----KLDGDI 222
 V I N + + +NG K+ SN + D EVI N E I+ + +G +
 Sbjct: 10 VVICNEVVSEEVNVGVKVVSNNEFIDNNEVINNNEFIYNNGVVGNFYSENKVVARDNGFV 69

Query: 223 DRTQFIWMKYFSIFNTELSQS-----NIEERYKIQSYSEYLKDFWGNPLMYNKEYMFN 276
 F E+I N +S S ++ K+ +Y , N +Y N E X
 Sbjct: 70 SNIGFGNSNGFNIGNNDVVGSGSWCVDNEVDNNNKVVNY-----NGFIYNNEVYNNE 120

Query: 277 AGNKNSYIK---LKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSIND 332
 N N ++ + D E++ N + + + + +N ND
 Sbjct: 121 IVNNNEFVNNNGFIYNDVRDHEVVNNNDVVFYNDDEVVRDNGFIYNNNEVV---NNNVVFYND 177

Query: 333 DIVRKEDYIYLDFFNLNQ 350

+ N +I+ +N+ F N +NN ++T+G L N D + D S+ NG
 Sbjct: 194 IYLNNSNIEINGDAMLMNQSI F---NTMNNLDLFISGLHLNDDSLFLFDNNEMTING 249

Query: 213 EII 215
 +++
 Sbjct: 250 DLL 252

tr Q7RTC2	Hypothetical protein (Fragment) [PY00072] [Plasmodium	3663
Q7RTC2_PLAYO	yoelii	AA
	yoelii]	<u>align</u>

Score = 41.6 bits (96), Expect = 0.037
 Identities = 66/310 (21%), Positives = 125/310 (40%), Gaps = 77/310 (24%)

Query: 45 KDNNLIDLSGYGAKVEVYDGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFDFSVF 104
 KDN ++ + ++ EV +GV++ N+F N +I N+ F+
 Sbjct: 6 KDNNEVVICNEVVSEEVNVGVKVVSNNF-----IDNNEVINNNEFI----- 47

Query: 105 WIRIPKYKNDGIQN-YIHNEYTIINCMKNNSGWKISIR---GNRII---WTL---IDIN 153
 Y N + N Y N+ N +N G+ S GN ++ W + +D N
 Sbjct: 48 -----YNNGVVGNFYSENKVVARDNGFVSNIGFGNSNGFNIGNDVSGSWCVDNEVDNN 101

Query: 154 GKTKSV-FFEYNIREDISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANG 212
 K + F YN +E +N FV NN IY D+D + N
 Sbjct: 102 NKVVNYNGFIYNNNEVYNNEIVNNNEFVN-----NNGFIY-----NDVRD--HEVVNN 146

Query: 213 EIIFKLDGDIDRTQFIWMKYFSIFNTELSQSIEERYKIQSSEYLKDFWGNPLMYNKEY 272
 +++F D + F I+N E+ +N+ + E +D N YN E
 Sbjct: 147 DVVFYNDDEVVRDNGF-----IYNNEVNNNNV-----VFYNEIVRD---NGFFYNDEV 191

Query: 273 YMFnAGNKNNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSIND 332
 N N + + E+++ S++ N++ +N + +Y GE +N++++ +
 Sbjct: 192 -----NNNEVVNNNEVSDNEVSDSEFIYNNNEVNNNEVYNGEVV-----NNNEAVQN 240

Query: 333 DIVRKEDYIY 342
 +--- +Y
 Sbjct: 241 GVIKNYGLMY 250

Score = 36.2 bits (82), Expect = 1.6
 Identities = 44/198 (22%), Positives = 73/198 (36%), Gaps = 38/198 (19%)

Query: 179 VTITNNLNNAKIYING-KLESNTDIKDIREVIANGEIIF-----KLDGDI 222
 V I N + + +NG K+ SN + D EVI N E I+ + +G +
 Sbjct: 10 VVICNEVVSEEVNVGVKVVSNNFIDNNEVINNNEFIYNNNGVGNFYSENKVVARDNGFV 69

Query: 223 DRTQFIWMKYFSIFNTELSQS-----NIEERYKIQSSEYLKDFWGNPLMYNKEYMFN 276
 F E+I N +S S + + K+ +Y N +Y N X
 Sbjct: 70 SNIGFGNSNGFNIGNDVSGSWCVDNEVDNNNKVVNY-----NGFIYNNNEVYNNE 120

Query: 277 AGNKNSYIK---LKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSIND 332
 N N + + + D E++ N + + + + +N ND
 Sbjct: 121 IVNNNEFVNNNGFIYNDVRDHEVVNNNDVFYNDDEVVRDNGFIYNNNEVV---NNNVVFYND 177

Query: 333 DIVRKEDYIYLDFFNLNQ 350

+IVR + Y D N N+
 Sbjct: 178 EIVRDNGFFYNDEVNNNE 195

tr Q7RFF5 Arabinogalactan protein [PY04751] [Plasmodium yoelii] 378
 Q7RFF5_PLAYO yoelii] AA align

Score = 40.8 bits (94), Expect = 0.064
 Identities = 42/176 (23%), Positives = 80/176 (44%), Gaps = 20/176 (11%)

Query: 182 TNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRT---QFIWMKYFSIFNT 238
 + N NN+ +N K+ DT+ + +I N + K D +++ Q I+ S ++
 Sbjct: 104 SENSNNSDNVLNNKI---DIEKDKNIIVNKSDL-KDDDNLNTKKMDQIIYKSIQSINYDK 158

Query: 239 EL-SQSNIIEERYKIQSYSEYLKDFW---GNPLMYNKEYY--MFNA---GNKNSYIKLK 287
 E +++N+++ Y++ X++ K++ NP K YY + N+ GN+
 Sbjct: 159 EFFAKNNLQEELYQLH-YNKLSKEYEFFEDDPYKNKKCYYGNISNSDKIRGNEQYINNSN 217

Query: 288 KDSPVGELTRSKYQNQSKYINYRDLYIGEKFIIIRKSNSQSINDDIVRKEDYIYL 343
 +S + + N KY + D+ + + K N+ S ND K D++YL
 Sbjct: 218 SESEINSDYDSNDSNFKKKYYEFNDIDFDQIYKYIYKKNNVSENDFKFKRDHLYL 273

tr Q8ILN7 Hypothetical protein [PF14_0206] [Plasmodium falciparum] 910
 Q8ILN7_PLAF7 (isolate AA align
 3D7)]

Score = 40.4 bits (93), Expect = 0.083
 Identities = 55/278 (19%), Positives = 106/278 (37%), Gaps = 53/278 (19%)

Query: 75 LTSSANSKIRVTQNQNIIFNSVFLDFSVSFWRIPKYKNDGIQNYIHNEYTIINCMKNNS 134
 + +--+N I +N NEE+ +F + ND YTH++ + N
 Sbjct: 347 IDNNNSNVMIHFNKNDNIIYKDIFKKLDEERKQKKDNIYNDYAHKYIHSDMLYNYRVVQND 406

Query: 135 GWKISIRGNRIIWTLIDINGKTGSVFFEYNIREDISEYINRWFVTITNNLNNAKIYING 194
 +KI I L +N +FF N+ +DI++ + ++
 Sbjct: 407 LYKI-----IQPVLYNLN----IFFNQNVIKDINKIMEKY----- 437

Query: 195 KLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIIEERYKIQSY 254
 +T I+D++V S +++ +++ + X E+ Q+N+ +
 Sbjct: 438 ----DTVIQDVQQVGRKKEYNKRINEGLEKREGHKSTYEK--ENEVKQNNVTQNGD---- 487

Query: 255 SEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNS----- 305
 K N Y +EX N N+ I KK K M +
 Sbjct: 488 ----KKLQNNVQTYEQEYIQTNLHNDDKNINTKKIQNSKNYHVNEKRNDKNVDNKNKDKE 543

Query: 306 KYINYRDLYIGEKFIIIRR-KSNSQSINDDIVRKEDYIY 342
 + INY +E G+K I+ K + + + RKE+ ++
 Sbjct: 544 ECINYTELDKGDKHIMNTLKIPNNKMQKEEKRKENVL 581

tr Q8I462 Hypothetical protein PFE0190c [PFE0190c] [Plasmodium] 662

+IVR + Y D N N+
 Sbjct: 178 EIVRDNGFFYNDEVNNNE 195

tr Q7RFF5 Arabinogalactan protein [PY04751] [Plasmodium yoelii] 378
Q7RFF5_PLAYO yoelii] AA
align

Score = 40.8 bits (94), Expect = 0.064
 Identities = 42/176 (23%), Positives = 80/176 (44%), Gaps = 20/176 (11%)

Query: 182 TNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGIDRT---QFIWMKYFSIFNT 238
 + N NN+ +N K+ DT+ + I N + K D +++ Q I+ S ++
 Sbjct: 104 SENSNNSDNVLNNKI---DIEKDKNIIVNKSDL-KDDDNLNTKKMDQIIYKSIQSINYDK 158

Query: 239 EL-SQSNIIEERYKIQSYSEYLKDFW---GNPLMYNKEYY--MFNA---GNKNSYIKLK 287
 E +--+N++E Y++ Y++ K++ NP K YY + N+ GN+
 Sbjct: 159 EFFAKNNLQEYQLH-YNKLKEYEFFEDDPYKNKKCYYGNISNSDKIRGNEQYINNSN 217

Query: 288 KDSPVGELTRSKYQNQSKYINYRDLYIGEKFIIIRRKNSQSINDDIVRKEDYIYL 343
 +S + + N KY + D+ + + K N+ S ND K D++YL
 Sbjct: 218 SESEINSDYDSNDSNFKKKYYEFNDIDFDQIYKYIYKKNNVSENDFKFKRDHLYL 273

tr Q8ILN7 Hypothetical protein [PF14_0206] [Plasmodium falciparum] 910
Q8ILN7_PLAF7 (isolate AA
3D7)] align

Score = 40.4 bits (93), Expect = 0.083
 Identities = 55/278 (19%), Positives = 106/278 (37%), Gaps = 53/278 (19%)

Query: 75 LTSSANSKIRVTQNQNIIFNSVFLDFSVFWIRIPKYKNDGIQNYIHNEYTIINC MKNNS 134
 + +--+N I +N NII+ +F + ND YI+ + + N
 Sbjct: 347 IDNNNSNVMIHFNKNDNIIYKDIFKKLDEERKQKKDNIYNDYAHKYIHSDMLYNYRVVQND 406

Query: 135 GWKISIRGNRIIWTLIDINGKTGSVFFEYNIREDISEYINRWFVTITNNLNNAKIYING 194
 +KI I L +N +FF N+ +DI++ + ++
 Sbjct: 407 LYKI-----IQPVLVNLN----IFFNQNVIKDINKIMEKY----- 437

Query: 195 KLESNTDIKDIREVIANGEIIFKLDGIDRTQFIWMKYFSIFNTLSQSNIIEERYKIQSY 254
 +P I+D+-+V E +--+ +--+ + X E+ Q+N+ +
 Sbjct: 438 ----DTVIQDVQQVGRKKEYNKRINEGLEKREGHKSTYEK--ENEVKQNNVTQNGD---- 487

Query: 255 SEYLKDFWGNPLMYNKEYYMFNAGNKNYSIKLKKDSPVGEILTRSKYNQNS----- 305
 K N Y +EY N N + I KK K N +
 Sbjct: 488 ----KKLQNNVQTYEQEYIQTNLHNDDKNINTKKIQNSKNYHVNEKRNDKNVDNKNDKE 543

Query: 306 KYINYRDLYIGEKFIIIRR-KSNSQSINDDIVRKEDYIY 342
 + I NY +L G+K I+ K + + + RKE+ ++
 Sbjct: 544 ECINYTELDKGDKHIMNTLKI PNNKMQKEEKRKENVLF 581

tr Q8I462 Hypothetical protein PFE0190c [PFE0190c] [Plasmodium] 662

Q8I462_PLAF7 **falciparum**
 (isolate 3D7)] AA
align
 Score = 40.4 bits (93), Expect = 0.083
 Identities = 44/204 (21%), Positives = 78/204 (37%), Gaps = 27/204 (13%)
 Query: 98 LDFSWSFWIRIPKYKNDGQNYIHNEYT-----IINCMKNNSGWKISIRGNRIIW 147
 +D+ + + I + K D + N + E INN +++ I++ +R
 Sbjct: 94 VDYHLQYVSNIFEKKKDELNNIMEKEKKSMSIDEPLICDIINYLESVINGNINVNDHRFNH 153
 Query: 148 TLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNNL-NAKIYINGKLESNTDIKDIR 206
 T+I K + NT +I+ IN I NN+ NN IN +N DT
 Sbjct: 154 NNINIYNKDHIISNININNNINNNINNNINNNINNNINNNINNNINNNINNNNNNNDDISLDN 213
 Query: 207 EVIANGEIIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNEERYKIQSYSEYLKDFWGNPL 266
 + G + I+ + YF F E + N++ + S + + +
 Sbjct: 214 KCSGGGSFLKNLN-----LSYFKDFLVERKKINLDALFDNDNSLNVLFDELY---- 259
 Query: 267 MYNKEYYMFNAGNKN--SYIKLKK 288
 Y Y + N N +TK+K+
 Sbjct: 260 TYTYIYLLINYKRNNFFDFIKMKR 283

tr Q7RRG0 Protein kinase domain, putative [PY00761] [Plasmodium 2941
 Q7RRG0_PLAYO yoelii yoelii] AA align

 Score = 40.4 bits (93), Expect = 0.083
 Identities = 85/409 (20%), Positives = 151/409 (36%), Gaps = 105/409 (25%)

 Query: 64 GVELNDKNQFKLTSSANSKIRVTQNQNIIFN---SVFLDFSVSFWIRIPKYKNDGIQNY 119
 G+ +N + AN K+ NI+ N ++ L + ++ I GI+N
 Sbjct: 1720 GINMNTNGTVNRNTVANYKVN----NILINDKLKNILLSKNFDHFL-IEHENENKIGIRNS 1773

 Query: 120 IHNEYTIINCMK--NNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNI-----RED 168
 I+N Y+ + NN+G + GN NG V + NI +E
 Sbjct: 1774 INNSYSNTGNVNHNNNAGRTVGANGNCTSNECTPNGTNIGVLKDSNILSGNMPKLKES 1833

 Query: 169 ISEYINRWFVTITNNLNNAKIYINGKLESNTDIKIREVIANGEIIFKLDGDIDRTQFI 228
 + Y + + NN+ N KI N ++ NT+ I+ T+R
 Sbjct: 1834 YNYYSHFKSQIIPSNNNVINKKITENTEISENTENNPKIQ-----GINR---- 1875

 Query: 229 WMKYFSIFNTELSQSNIIEERYKIQSYSEYLKDFWGNPLMYNKE-YYMFNAGNKNSYIKLK 287
 I+N + Q N +E + EY + NK ++ KA N +YI+
 Sbjct: 1876 -----IYNNYIGQGNTKENIPMVNKEYSNKHISD--INKSIFFSQNANNSLNYIE-- 1924

 Query: 288 KDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRR--KSNSQSINDDIVRKEDYIYLD 345
 S Y Y + K IRR K+ ++ND+++
 Sbjct: 1925 -----SVNIYIPSSLLNSKNKIRRDGKTCGTNLNDNLINMH----- 1960

 Query: 346 FNLNQEWRVYTXXXXXXXXXXXXXXAPISDSDEFYNTIQIKEYDEQP---TYSQOLLFKK 401
 NQ+ ++Y I + +++YN I I+E + + L+K+
 Sbjct: 1961 ---NQQRQIY-----QIENENKYYNNINIQEGINKKIANLNFQDILYKQ 2002

 Query: 402 DEESTDEIGLIGIHRFYYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKL 450
 + + D+I + Y+S F Y + I+ K + R+ N K+
 Sbjct: 2003 NNLNIDQIN---KKKYDSN--FNNYLNSTAITSISNKNIPROFTNAKI 2045

Q8I462_PLAF7 falciparum
 (isolate 3D7)] AA
align
 Score = 40.4 bits (93), Expect = 0.083
 Identities = 44/204 (21%), Positives = 78/204 (37%), Gaps = 27/204 (13%)
 Query: 98 LDFSVSFWIRIPKYKNDGIQNYIHNEYT-----IINCMKNNSGWKISIRGNRIIW 147
 +D+ + + I + K D + N + R IIN +++ I++ +R
 Sbjct: 94 VDYHLQYVSNIFEKKDELNNIMEKEKKSMSIDEPLICDIINYLESVINGNINVVDNHRFNH 153
 Query: 148 TLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNNL-NNAKIYINGKLESNTDIKDIR 206
 T+I K + MI +I+ IN T NN+ NN IN +N DT
 Sbjct: 154 NNINIYNKDHIISNININNNINNNINNNINNNINNNINNNINNNINNNNNNNDDISLDN 213
 Query: 207 EVIANGEIIIFKLDGIDRTQFIWMKYFSIFNTELSQSNIERYKIQSSEYLKDFWGNPL 266
 + G + L+ + YF F E + N++ + S + + +
 Sbjct: 214 KCSGGGSFLKNLN-----LSYFKDFLVERKKINLDALFNDNSLNVLFDELY---- 259
 Query: 267 MYNKEYYMFMAGNKN--SYIKLKK 288
 Y X + N N +TK+K+
 Sbjct: 260 TYTYIYLLINYKRNNFFDFIKMKR 283

tr Q7RRG0 Protein kinase domain, putative [PY00761] [Plasmodium 2941
 Q7RRG0_PLAYO yoelii yoelii] AA
align

Score = 40.4 bits (93), Expect = 0.083
 Identities = 85/409 (20%), Positives = 151/409 (36%), Gaps = 105/409 (25%)

Query: 64 GVELNDKNQFKLTSSANSKIRVTQNQNIIFN---SVFLDFSVSFWRIPKYKNDGIQNY 119
 + N + AN K+ NI+ N ++ L + ++ I GI+N
 Sbjct: 1720 GINMNTNGTVNRNTVANYKVN----NILINDKLKNILLSKNFDHFL-IEENENKIGIRNS 1773

Query: 120 IHNEYTIINCMK--NNSGWKISIRGNRIIWTLIDINGKTKSVFSEYNI-----RED 168
 I+AN Y+ + NN+G + GN NG V + NI + E
 Sbjct: 1774 INNSYSNTGNVNHNNNAGRTVGANGNCTSNECTPNGTNIGVLKDSNILSGNMPKLKES 1833

Query: 169 ISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFI 228
 + Y + + NN+ N KI N ++ NT+ I+ T+R
 Sbjct: 1834 YNYYSHFKSQIIPSNNNVINKKITENTEISENTENNKIQ-----GINR---- 1875

Query: 229 WMKYFSIFNTELSQSNIIEERYKIQSYSEYLKDFWGNPLMYNKE-YYMFNAGNKNSYIKLK 287
 I+N + Q R + E + BY + NK ++ NA N + YI+
 Sbjct: 1876 -----IYNNYIGQGNTKENIPMVNKEYSNKHISD--INKSIFFSQNANNSLNYIE-- 1924

Query: 288 KDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRR--KSNSQSINDDIVRKEDYIYLD 345
 S Y Y + K IRR K+ ++ND++
 Sbjct: 1925 -----SVNIYIPSSLLNSKNKIRRDGKTCGTNLNDNLINMH----- 1960

Query: 346 FNLNQEWRVYTXXXXXXXXXXXXXXAPISDSDEFYNTIQIKEYDEQP---TYSQQLLFKK 401
 NQ+ ++Y I + +++YN I I+E + + L+K+
 Sbjct: 1961 ---NQQRQIY-----QIENENKYYNNINIQEGINKKIANLNFQDILYKQ 2002

Query: 402 DEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKL 450
 + + D+I + Y+S F Y + I+ K + R+ N K+
 Sbjct: 2003 NNLNIDQIN---KKKYDSN--FNNYLNSTAITSISNKNI PRQFTNAKI 2045

tr Q7RPW6 Hypothetical protein (Fragment) [PY01338] [Plasmodium 3644
Q7RPW6_PLAYO yoelii yoelii] AA
align

Score = 40.4 bits (93), Expect = 0.083
 Identities = 69/315 (21%), Positives = 134/315 (41%), Gaps = 33/315 (10%)

Query: 3 NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXRYKDNNLIDLSGYG-AKVEV 61
 NKY+ I ++ND ++ E + + + R ++N+ + + Y +K+E
 Sbjct: 3012 NKYISKIN---IKHSNDILMYEKEHTGSLDNISHQSTDRAKNNNDNIENENHYNNSKLE- 3066

Query: 62 YDGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLLDFSVSFWRIPKYKNDGIQNYIH 121
 ++W K +++ +R +N+ +F ++ + I I N+ N+ +++
 Sbjct: 3067 --NSQINPKEDNNNTLNNSIYMLRKQKNEKKLFELYIYIYII--IHIIFYNE---SFVD 3119

Query: 122 NEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIRE--DISEYINRWFFV 179
 +Y I NC+ I + I + N K+ S + +N E DI+E+I+ +
 Sbjct: 3120 LKYYIYNCI-----CEIASSYIPFYFTQNNIKSFSYYSNHNSEENKDINEFISFINNI 3172

Query: 180 TITNNLNAKIY--INGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFN 237
 I+ N+N+ K+Y N K E K I + N + + +FT +
 Sbjct: 3173 NISTNVNDLKLYNFNNKKKEKKLKSKKILKTYNSDNENDHHTQASKLEFIQSPKSA--- 3229

Query: 238 TELSQSNIEERYKIQSYSEYL--KDEFGNPLMYNKEYMFNAGNK---NSYIKLKKDSP 291
 T+ + N S S ++ + F N + Y + N+ N+ NS I+ KK+S
 Sbjct: 3230 TKTYEENEYSEIPGSSISTFIGTEKFSSNESGIERIYNLSNSKNERIENNNSCIEQQKNSR 3289

Query: 292 VGEILTRSKYNQNSK 306
 I T+ K QN +
 Sbjct: 3290 SICIDTKLKNIQNPR 3304

Score = 40.0 bits (92), Expect = 0.11
 Identities = 69/332 (20%), Positives = 124/332 (36%), Gaps = 71/332 (21%)

Query: 55 YGAKVEVYDGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLLDFSVSFWRIPKYKND 114
 Y + + + + N+ + + N N + N+ F+ + + + + YKN+
 Sbjct: 353 YNDQYVISNYIKQNNEIEVITTDGRRNNTSLVNLQKLKNNNFIKNNHTIYTKPIIYKNN 412

Query: 115 GIQN-----YIHNEYTIINCM-----KNNSGWKI---SIRGNRIIWTL 149
 + N YI N+ +N K+ G I S G+RIL
 Sbjct: 413 KLYNSNYIINQNLEYIYQNDVNNMNTSNIHKIVRENIPPKSQDGPFINETSNLGSRII--- 469

Query: 150 IDINGKTKSVFFEYNIREDISEYINRWFFVTI-----TNNLNAKIY 191
 NG + ++ N+ + + IN + TNN+N I
 Sbjct: 470 ---NGNASTSLYDKNVENNNANNINSALNTNVDLKFHSKTGISNLHVKNCTNNINKLMS 526

Query: 192 INGKLESNTDIKDIREVIANGEIIFKLDGDIDRT---QFIWMKYFSIFNTLSQNSI-EE 247
 K E+ ++K+ + + + I G+I T W ++ N S +N+ +E
 Sbjct: 527 YRNKEEAKENVNVKKETYINDINSSNGGNIINTIASNMKWNNNSNMINNIAASMNNINKE 586

Query: 248 RYKIQSYSEYLKDFWGNPLMYNKEYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKY 307
 ++ I+ K + N +YN + M + N N LK + P K N N
 Sbjct: 587 KHWIK-----KTYLDNTDIYNAD-KMSVSSNMNKLYDLKNEKP-----KKNNNDLN 631

tr Q7RPW6 Hypothetical protein (Fragment) [PY01338] [Plasmodium 3644
Q7RPW6_PLAYO yoelii yoelii] AA
align

Score = 40.4 bits (93), Expect = 0.083
 Identities = 69/315 (21%), Positives = 134/315 (41%), Gaps = 33/315 (10%)

Query: 3 NKYLKTIMPFDSL IYTNDTILIE MFNKYNSE XXXXXXXXRYKDNNLIDL SGYG-AKVEV 61
 NKY+ I ++ND ++ E + + + R ++N+ + + Y +K+E
 Sbjct: 3012 NKYISKIN---IKHSNDIL MYEKEHTGS LDNISHQSTDDRKNNDNIENENHYNNSKLE- 3066

Query: 62 YDGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSF WIRIPKYKNDG IQNYIH 121
 ++W K +++ +R +N+ +F ++ + I I K+ N+ +++
 Sbjct: 3067 --NSQINPKEDNNNTLNN SIYMLRKQKNEKKLFELYIYIYI--IHIIFYNE---SFVD 3119

Query: 122 NEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIRE--DISEYINRWFFV 179
 +Y I NC+ I + I + N K+ S + +N E D+E+I+ +
 Sbjct: 3120 LKYYIYNCI-----CEIASSYIPFYFTQNNIKSFSYYSNHNSEENKDINEFISFINNI 3172

Query: 180 TITNNLNAKIY--INGKLESNTDIKDIR E VIANGEIIFKLDGDIDRTQFIWMKYFSIFN 237
 I+ N+N+ K+Y N K E K T + N + + +FT +
 Sbjct: 3173 NISTNVNDLKLYNFNNKKKEKKLKS K KTKYNSDNENDHHTQASKLEFIQSPKSA--- 3229

Query: 238 TELSQSNIEERYKIQSYSEYL--KDFWGPNPLMYNKEYMFNAGNK---NSYIKLKKDSP 291
 T+ + N S S ++ + F N + Y + N+ N+ NS I+ KK+S
 Sbjct: 3230 TKTYEENEYSEIPGSSISTFIGTEKFSSNESGIERIYNLNSNSKNERIENN CIEQKKNSR 3289

Query: 292 VGEILTRSKYNQNSK 306
 I T+ K QN +
 Sbjct: 3290 SICIDTKLKNIQNPR 3304

Score = 40.0 bits (92), Expect = 0.11
 Identities = 69/332 (20%), Positives = 124/332 (36%), Gaps = 71/332 (21%)

Query: 55 YGAKVEVYDGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSF WIRIPKYKND 114
 Y + + + + N+ +T+ N N + N+ F+ + + + + YKN+
 Sbjct: 353 YNDQYVISNYIKQNNNEIEVIITDGNRNNTSLVNLQKLKNNNFIKNNHTIYT KPIIYKNN 412

Query: 115 GIQN-----YIHNEYTIINCM-----KNNSGWKI---SIRGNRIIWTL 149
 + N YI N+ +N K+ G T S G+R I
 Sbjct: 413 KLYNSNYIINQNLEYIYQNDVNNMNTSNIHKIVRENIPPKSQDGPFINETS NLGSRII--- 469

Query: 150 IDINGKTKSVFFEYNIRE DISEYINRWFFVTI-----TNNLNAKIY 191
 NG + ++ N+ + + IN + TNN+N I
 Sbjct: 470 ---NGNASTSLYDKNVENNANNINSALNTVDLKFHSKTGISNLHVVKNTNNINKL MIS 526

Query: 192 INGKLESNTDIKDIR E VIANGEIIFKLDGDIDRT---QFIWMKYFSIFNTELSQSNI-EE 247
 K E+ ++K+ + + + I G+I T W ++ N S +N+ +E
 Sbjct: 527 YRNKEEAKENVNVKKETYINDINSSNGNIINTIASNMKWNNNSNMINNIA SMNNINKE 586

Query: 248 RYKIQSYSEYLKDFWGNPLMYNKEYMFNAGNKNSYIKLKKDSP VGEILTRSKYNQNSKY 307
 ++ I+ K+ N +YN + M + N N I K + P K N N
 Sbjct: 587 KHWIK-----KTYLDNTDIYNAD-KMSVSSNMNKLYDLKNEKP-----KKNNNDLN 631

Query: 308 INYRDLYIGEKFIIIRRKSNSQSINDDIVRKED 339

IN D+ I + + NS N+ + K D

Sbjct: 632 INNTDMVINSR---KCSENSTENNNRQIMKND 660

Score = 36.2 bits (82), Expect = 1.6

Identities = 42/168 (25%), Positives = 72/168 (42%), Gaps = 16/168 (9%)

Query: 19 NDTILIEMFNKYNSEXXXXXXXXXRYKDNNLIDLGYGAKVEVDGV-ELNDKNQFKLTS 77

NDMF I + N+Y ++ D NL+ K+ +DG+ +I D+ + +

Sbjct: 823 NDTTNINLSNQYINKNFMPTHIIN--DDENLLG---STKMSSFDGITKLEDEKNIEYLT 876

Query: 78 SANSKIRVTQNQNIIFNSVFLDFSVFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWK 137

I +N ++N+ ++ KYK D + I+N+ +N N +

Sbjct: 877 GEYYYINGKMEENKLYNNENINC-----FRKYK-DMLNTNINNEKYNVNGKYNRRNLS 928

Query: 138 ISIRGNRIIWTL-IDINGKTKSVFFEYNIREDISEYIINRWFFVTITNN 184

S+ N T I NGK KS +YN++ ++ +N F+ I NN

Sbjct: 929 PSVNINDKANTKNITENGKYKSYQKDYNLKTFKNKSVPQSFLQIKNN 976

sp P21358 Mitochondrial ribosomal protein VAR1 [VAR1] [Candida 339
RMAR_CANGA glabrata AA
(Yeast) (Torulopsis glabrata)] align

Score = 40.0 bits (92), Expect = 0.11

Identities = 71/314 (22%), Positives = 118/314 (36%), Gaps = 58/314 (18%)

Query: 28 NKYNSEXXXXXXXXXRYKDNNLIDLGYGAK---VEVYDGVELNDKNQFKLTSSANSKI 83

NKY SE + N L Y + Y +L +K +KL S N+K I

Sbjct: 41 NKYLSELNNKGNSLQHLNNMNNWKLQNYNYNKNNTINNYINSKLINKLLYKLMSLKNKI 100

Query: 84 RVTQ----NQNII-----FNSVFLDFSVFWIRIPKYKN-----DGIQNYIH 121

+++ N N+I N+ + ++ + I K N I +Y +

Sbjct: 101 IISKPLYKINMNVINIRFYYYNMNNYNNNIYYINMINKLMRNLNINMNNLSNILSYYY 160

Query: 122 NEYTIINCMKNNSGWKISIRGNRIIW---TLIDINGKTKSVFFEY----NIREDISEYI 173

N+ II +K K N I+ +L+D N + EY NT ++++

Sbjct: 161 NKKVIIIEPIK---LKLYNNNEIMTKYISLLDNKYNNGLLMEQRTLNNIMPKLDHN 216

Query: 174 NRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIFFKLDGDIDRTQFIWMKYF 233

++ NN+N K Y N I +N +I +I I + + + + F + + +

Sbjct: 217 ISMNYINNNINNINKLK-YNNILLNNNNNNNNIYNNI-----NINNNMNLLMFKYLIGW 268

Query: 234 SIFNTELSQSNIIEERYKIQSYSEYLKDFWGNPLMYNKEYMFNAGNKNNSYIKLKKDSPVG 293

ST NI S + N NK+Y GN N+ KI +

Sbjct: 269 SIMLKGRNLKNI-----SRISTTYLNNGTFNNKKYLW---GNLNNNFKLNYINSNN 316

Query: 294 EILTRSKYNQNSKY 307

I + N+N KY

Sbjct: 317 NIYNYNNINKNGKY 330

tr Q8II48 Hypothetical protein [PF11_0326] [Plasmodium falciparum] 2763

Query: 308 INYRDLYIGEKFIIRRKSNSQSINDDIVRKED 339

EN D+ E + + NS N+ + K D

Sbjct: 632 INNTDMVINSR---KSENSTENNNRQIMKND 660

Score = 36.2 bits (82), Expect = 1.6

Identities = 42/168 (25%), Positives = 72/168 (42%), Gaps = 16/168 (9%)

Query: 19 NDTILIEMFNKYNSEXXXXXXXXXRYKDNNLIDLSGYGAKVEVYDGV-ELNDKNQFKLTS 77

NDT I + N+Y ++ D NL+ K+ +DG+ +L D+ + +

Sbjct: 823 NDTTNINLSNQYINKNFMPTHIIN--DDENLLG---STKMSSFDGITKLEDEKNIEYLT 876

Query: 78 SANSKIRVTQNQNIIFNSVFLDFSVFWIRIPKYKNDGIQNYIHNEYTIINC MKNNSGWK 137

I +N ++N+ ++ KYK D + I+NE +N N +

Sbjct: 877 GEYYYINGKMEENKLYNNENINC-----FRKYK-DMLNTNINNEKYNVNGKYNRRNLS 928

Query: 138 ISIRGNRIIWTL-IDINGKTCSVFFEYNIREDISEYIINRWFFVTITNN 184

S+ N T T NGK KS +YN++ ++ +N F+ I NN

Sbjct: 929 PSVNINDKANTKNITENGKYKSYQKDYNLKTFKNKSVNPQSFLQIKNN 976

sp P21358 Mitochondrial ribosomal protein VAR1 [VAR1] [Candida
RMAR_CANGA glabrata AA
(Yeast) (Torulopsis glabrata)] align

Score = 40.0 bits (92), Expect = 0.11

Identities = 71/314 (22%), Positives = 118/314 (36%), Gaps = 58/314 (18%)

Query: 28 NKYNSEXXXXXXXXXRYKDNNLIDLSGYGAK---VEVYDGVELNDKNQFKLTSSANSKI 83

NKY SE + N L Y + Y +L +K +KL S N+KT

Sbjct: 41 NKYLSELNNKGNSLQHLNNMNNWKLQNYNPKNNNTINNYINSKLINKLLYKLMSLKNNKI 100

Query: 84 RVTQ----NQNII-----FNSVFLDFSVFWIRIPKYKN-----DGIQNYIH 121

+++ N N+I N+ + ++ + I K N I +Y +

Sbjct: 101 IISKPLYKINMNVINIRFYNNMNNYNNNIIYINMINKLMNRNINMNNLSNILSYYY 160

Query: 122 NEYTIINC MKNNSGWKISIRGNRIIW---TLIDINGKTCSVFFEY----NIREDISEYI 173

N+ II +K K N I+ +L+D N + EY NI ++++

Sbjct: 161 NKKVIEPIK---LKLYNNNEIMTKYISLLDNKYNNGLLMEQRTLNNIMPKLNDHN 216

Query: 174 NRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYF 233

++ NN+N K Y N L +N +I +I I + + + + F + + +

Sbjct: 217 ISMNYINNNINNINKL-K-YNNILLNNNNNINNIIYNNI-----NINNNMNLLMFKYLIGW 268

Query: 234 SIFNTELSQSNIIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNNSYIKLKKDSPVG 293

ST NI S + N NK+Y GN N+ KI +

Sbjct: 269 SIMLKGRNLKNI-----SRISTTYLNNGTFNNKKYLW---GNLNNNFKLNYINSNN 316

Query: 294 EILTRSKYNQNSKY 307

I + N+N KY

Sbjct: 317 NIYNYNINNKNGKY 330

tr Q8II48 Hypothetical protein [PF11_0326] [Plasmodium falciparum] 2763

Q8II48_PLAF7 (isolate 3D7)] AA align

Score = 40.0 bits (92), Expect = 0.11
 Identities = 67/278 (24%), Positives = 119/278 (42%), Gaps = 33/278 (11%)

Query: 46 DNNLIDLSGYGAKVEVYDGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFW 105
 D+N D + Y Y+ N+E K + +K + +N+ I+ SVF + +

Sbjct: 537 DSNDDDDNNNYYYYSNNNNYRNNKNNFKRNNFEINKEK--ENKEKIYTSVFEENNKK--- 591

Query: 106 IRIPKYKNDGIQNYIH-NEYTIINC MKNNSGWKISIRGNRIIWTLDIN-GKTKSVFFEY 163
 + T N N+I+ NE K+N I + + IDI+ K ++FF++

Sbjct: 592 VIIDMINNKNKDNFININE-----KSNEITNIHNYTDVYVDEDIDIHVDKNNNIFFDH 644

Query: 164 NIREDISEYINRWFFVTITNNLNNAKIYINGKL----ESNTDIKDIREVIANGEIIFKL 218
 N + ++ N + N + N + Y N KL E+N K+ + I E ++

Sbjct: 645 NSNFFVDDFNNLHVY----NKHNEEYYKNIKLYNRFMENNKTGKENYDYIQEYEYEY 699

Query: 219 DGDIDRTQFIWMKYFSIFNTELSQSNIER-YKIQSSEYLKDFWGNPLMYNKEYYMFA 277
 + D D + M Y I+N + +N + + I + Y + P M N + N

Sbjct: 700 E-DEDLSNNYNMDY--IYNDQIQRNNNDSQIIHDINNYDIF--SILSIPNMNNNDN---NN 751

Query: 278 GNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYI 315

N N ++ S ++N+ Y NY+D YI

Sbjct: 752 DNNNDNNNDNNNNNDNYYSSSSSKNNNYYNYQDRYI 789

tr **Q8I2R1** Hypothetical protein PFI1210w [PFI1210w] [Plasmodium 2082
Q8I2R1_PLAF7 falciparum AA
 (isolate 3D7)] align

Score = 40.0 bits (92), Expect = 0.11
 Identities = 55/287 (19%), Positives = 106/287 (36%), Gaps = 35/287 (12%)

Query: 65 VELNDKNQFKLTSSANSKIRVT-----QNQNIIFNSVFLDF-SVSFWIRIP 109
 + +ND + I: SS KI + + +N + ++ ++ + +S ++

Sbjct: 10 MNINDYEEKNLNSSGEKKINIIGDLASHNSGNFDEEKNSVCKNLIVNMPNISKGVQEE 69

Query: 110 KYKNDGIQNYIHNEYTIINC MKNNSGWKISIRGNRIIWTLDINGKTKSVFFEYNIREDI 169
 + K + + + NE +IN +K+ + G K E +

Sbjct: 70 ECKIEELDKVVRNEMDMINSLKDEK-----VIGMDKMYDMEKEKDMCL 112

Query: 170 SEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIW 229
 N + F N I+ + +N I + E N + + ID T+

Sbjct: 113 INEKNSYSFGKDKKKNNIDGIHNIHHISANDHIINPNEYKPNVQNLVSNSTHIDSTEICS 172

Query: 230 MKYFSIFNTELSQSNIERERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKK- 288
 K+ + ++ I Y E+ K + + N+ Y N N NS + L +

Sbjct: 173 SKFVKEEEHNNDNNEYDKNVHILKYPEHNKTMDMNNLSNQYLYSCNISNNNSQLHLSRL 232

Query: 289 -DSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIIRRKSNSQSINDDI 334

D E L K N K Y N ++ + + +IK SN+ + N++I

Sbjct: 233 FDKETDE-LNSIKVNNQDKYDNMSEIKLEKTLMIRDNSNNNNNNNN 278

Q8II48_PLAF7 (isolate 3D7)

AA align

Score = 40.0 bits (92), Expect = 0.11
 Identities = 67/278 (24%), Positives = 119/278 (42%), Gaps = 33/278 (11%)

Query: 46 DNNLIDLSGYGAKVEVYDGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFW 105
 D+N D + Y Y+ N+K+ K + +K+ +N+ I+ SV+ +
 Sbjct: 537 DSNDDDDNNNYYYYSNNYNNYRNNKNNFKRNNFEINKEK--ENKEKIYTSVFEENNKK--- 591

Query: 106 IRIPKYKNDGIQNYIH-NEYTIINC MKNNSGWKISIRGNRIIWTLIDIN-GTKTSVFFEY 163
 + I N N+I+ NE K+N I + + IDI+ K ++FF++
 Sbjct: 592 VIIDMINNKNKDNFININE-----KSNEITNIHNYTDVYVDEDIDIHVDKNNNIFDH 644

Query: 164 NIREDISEYINRWFFVTITNNLNNAKIYINGKL----ESNTDIKDIREVIANGEIIFKL 218
 N + ++ N + N +N + Y N KL E+N K+ + I E ++
 Sbjct: 645 NSNFFVDDFNNLHVY----NKHNEEYYKNIKLYNRFMENNKTGKENYDYIQEYEYEY 699

Query: 219 DGDIDRTQFIWMKYFSIFNTELSQSNIER-YKIQSSEYLKDFWGNPLMYNKEYYMFNA 277
 + D D + M Y I+N ++ +N + + I +Y + P M N + N
 Sbjct: 700 E-DEDLSNNYNMDY--IYNDQIQRNNDSQIIHDINNYDIF--SILSIPNMNNNDN---NN 751

Query: 278 GNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYI 315
 N N ++ S ++N+ Y NY+D YI
 Sbjct: 752 DNNNDNNNDNNNNNDNYYSSSSSKNNNYYNYQDRYI 789

tr Q8I2R1 Hypothetical protein PF11_1210w [PF11_1210w] [Plasmodium falciparum (isolate 3D7)] 2082
 AA align

Score = 40.0 bits (92), Expect = 0.11
 Identities = 55/287 (19%), Positives = 106/287 (36%), Gaps = 35/287 (12%)

Query: 65 VELNDKNQFKLTSSANSKIRVT-----QNQNIIFNSVFLDF-SVSFWIRIP 109
 + +ND + I: SS KI + + +N + ++ ++ ++S ++
 Sbjct: 10 MNINDYEEKNLNSSGEKKINIIGDLASHNSGNFDEEKNSVCKNLIVNMPNISKGVQEE 69

Query: 110 KYKNDGIQNYIHNEYTIINC MKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDI 169
 + K + + + NE +LN +K+ + G K E +
 Sbjct: 70 ECKIEELDKVVRNEMDMINSLKDEK-----VIGMDKMYDMEKEKDMCL 112

Query: 170 SEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLGDIDRTQFIW 229
 N + E N I+ + +N I + E N + + ID T+
 Sbjct: 113 INEKNSYSFGKDKKKNNIDGIHNIHHISANDHIINPNEYKPNVQNLVSNSTHIDSTEICS 172

Query: 230 MKYFSIFNTELSQSNIER YKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKK- 288
 E+ + ++ I Y E+ K + + N+ Y N N MS + S +
 Sbjct: 173 SKFVKEEEHNNDNNEYDKNVHILKYPEHNKT KDMDDNNLSNQYLYSCNISNNNSQLHLSRL 232

Query: 289 -DSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDI 334
 D E L K N KY N ++ + + +IR SN+ + N++I
 Sbjct: 233 FDKETDE-LNSIKVNNQDKYDNMSEIKLEKTLMIRDNSNNNNNNNNI 278

tr Q7RQ77 Hypothetical protein [PY01225] [Plasmodium yoelii] 3195
Q7RQ77_PLAYO yoelii] AA
align

Score = 40.0 bits (92), Expect = 0.11
 Identities = 63/259 (24%), Positives = 101/259 (38%), Gaps = 52/259 (20%)

Query: 110 KYKNDGIQNYIHNNEYTIINC--MKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIRE 167
 K N G+ H+ I NC N+ G ++I N +I+ + F+E +
 Sbjct: 787 KMSNWGMSLNHHDNININNNCDSFSNDKGNILNINNN-----EISDNNNTNFYEEEKKI 839

Query: 168 DISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEI-----FKLDGDI 222
 SE I++ + T N K + K E N + +I ++ +W I+ +KLD D+
 Sbjct: 840 FTSESIDKRGGLIEQTQINNVTKHYDIKKEENENYNNINDLSNKSIVSSKFSYKLDTDV 899

Query: 223 -----DR-----TQFIWMKYFSIFNTELSQSNIIEERYKIQSYSE 256
 D +F+ KY N E +Q+NI + +
 Sbjct: 900 LLKDSINFEKNDHINSLRKSNTDIIGYINKFVGSKYVEEGN-ETAQNNIRISGDTKIEDK 958

Query: 257 YLKDFWGNPLMYN-KEYYMF---NAGNKNSYIKL-KKDSPVGEILTRSKYN----QNS 305
 + + YN K Y MF N+N K K+S + +T YN +N
 Sbjct: 959 IIPIPMNDSRNEYNIKNYSMFGNKENNNQNHEDKLSKKESELFNCITNDIYNERKIYENE 1018

Query: 306 KYINYRDLYIGEKFIIIRRK 324
 Y+N DL + RR +K
 Sbjct: 1019 LYLNKDDLILNEKIFRDKK 1037

tr Q6LFH3 Hypothetical protein [PFF0460w] [Plasmodium falciparum] 987
Q6LFH3_PLAF7 (isolate
3D7)] AA
align

Score = 39.7 bits (91), Expect = 0.14
 Identities = 53/235 (22%), Positives = 96/235 (40%), Gaps = 32/235 (13%)

Query: 111 YKNDGIQNYIHNNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDIS 170
 YKN+ Y+ NE IN K +I+ + I+ + D N K K +YN +D +
 Sbjct: 177 YKNEEDCKYVINENKEINENK-----EINEINDNNIYNVDDNNNKYK---YKNNYDDNN 228

Query: 171 EYINRWFFVTITNNLNNAKIYINGKLESNTD---IKDIREVIANGE-----IIFK 217
 +Y F T + NN ++Y+ K +++ D +K+ + E +
 Sbjct: 229 KYYENAHFTNNCHTNKELYLLEKKQNDVDSLILKNEKNYKKENLNNNISPSCVIN 288

Query: 218 LDGDIDRTQFIWMKYFSIFNTELSQSNIIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNA 277
 DG+ +R + + + I E + EER +K + E+YM
 Sbjct: 289 KDGEBRNRSVSEPFIDIICKDE-EEKKEERTSQYHNQNEIKKINQKDVSVETEFYM--- 344

Query: 278 GNKNSYIKLKKDSPVGEILTRSKYN-QNSKYINYRDLYIGEKFIIIRRKSNSQSIN 331
 N+S + DS ++ +N +YIN + I K + KN + +N
 Sbjct: 345 --KDSLL---DSLEKLLIKNVSFNFVRKEYINIFEDMITSKRDVTWKKNNKEMN 393

sp Q98PH2 Mannitol-1-phosphate 5-dehydrogenase (EC 1.1.1.17) [mt1D] 360 AA
MT1D_MYCPU [Mycoplasma pulmonis] AA
align

tr Q7RQ77 Hypothetical protein [PY01225] [Plasmodium yoelii] 3195
Q7RQ77 _PLAYO yoelii] AA align

Score = 40.0 bits (92), Expect = 0.11
 Identities = 63/259 (24%), Positives = 101/259 (38%), Gaps = 52/259 (20%)

Query: 110 KYKNDGIQNYIHNEYTIINC--MKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIRE 167
 Sbjct: 787 KMSNWGMSLNHHDNININNNCDSFSNDKGNILNINNN-----EISDNNNTNFYEEKKI 839

Query: 168 DISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEII----FKLDGDI 222
 Sbjct: 840 FTSESIDKRGGLIEQTQINNVTKHLYDIKKEENENYNNINDLSNKSIVSSKFSYKLDTDV 899

Query: 223 -----DR-----TQFIWMKYFSIFNTELSQSNIERYKIQSYSE 256
 Sbjct: 900 LLKDSINFEKNDHINSLRKSNTDIIGYINKFVGSKYVEEGN-ETAQNNIRISGDTKIEDK 958

Query: 257 YLKDFWGNPLMYN-KEYYM-----NAGNKNSYIKL-KKDPVGEILTRSKYN----QNS 305
 Sbjct: 959 IIPIMNDSRNEYNIKNYSMFYGNKENNNQNHEDKLSKKESELFNCITNDIYNERKIYENE 1018

Query: 306 KYINYRDLYIGEKFIIRRK 324
 Sbjct: 1019 LYLNKDDLILNEKIFRDKK 1037

tr Q6LFH3 Hypothetical protein [PFF0460w] [Plasmodium falciparum] 987
Q6LFH3 _PLAF7 (isolate AA align
 3D7)]

Score = 39.7 bits (91), Expect = 0.14
 Identities = 53/235 (22%), Positives = 96/235 (40%), Gaps = 32/235 (13%)

Query: 111 YKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDIS 170
 Sbjct: 177 YKNEEDCKYVINENKEINENK-----EINEINDNNIYNVDDNNNKYK---YKNNYDDNN 228

Query: 171 EYINRWFFVTITNNLNNAKIYINGKLESNTD---IKDIREVIANGE-----IIFK 217
 Sbjct: 229 KYYENAHFTNNCHTNKELYLLEKKQNDVDSLILKNEKNVKKKENLNNNISPSCVIN 288

Query: 218 LDGDIDRTQFIWMKYFSIFNTELSQSNIERYKIQSYSEYLKDFWGNPLMYNKEYYMFA 277
 Sbjct: 289 KDGEBRNRSVSEPFIDIJKDE-EEKKKEERTSQYHNQNEIKKINQKDVSVETEFYM--- 344

Query: 278 GNKNSYIKLKKDSPVGEILTRSKYN-QNSKYINYRDLYIGEKFIIRRKNSQSIN 331
 Sbjct: 345 --KDSLL---DSLEKLLIKNVSFNFVRKEYINIFEDMITSKRDVTWKKNKEMN 393

sp Q98PH2 Mannitol-1-phosphate 5-dehydrogenase (EC 1.1.1.17) [mt1D] 360 AA
MT1D _MYCPU [Mycoplasma pulmonis] AA align

Score = 39.3 bits (90), Expect = 0.19
 Identities = 67/315 (21%), Positives = 123/315 (38%), Gaps = 69/315 (21%)

Query: 50 IDLSGYGAKVEVYDGVELNDK-----NQFKLTSSANSKIRVTQNQNIIFNSVFLDFSV 102
 T S + + ++ V+L +R N +K++S S + + N F++ SV
 Sbjct: 90 IGWSNLASLKKFFENVKLKEKAQIICFENGYKISSFFQSILNIDSNH-----FVNASH 142

Query: 103 SWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGTKSVFFE 162
 T F +K+D + Y+ + Y II KN S K++
 Sbjct: 143 DKII--PNFKSDSLDVYVESYYEIIILEQKNESQKKLNF----- 178

Query: 163 YNIREDISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDI 222
 N D+ YIN+ F+ N ++ I G L+ T I E + + +I+FK+
 Sbjct: 179 VNYSTDLEAYINKKLFLV---NAIHSTIGYLGYLKKYT---YINEALNDQQILFKIKRLA 232

Query: 223 DRTQFIWMKYFSIFNTLSQSNIE---ERYKIQSYSEYLKDFWGPNP---LMYNKEYYMFN 276
 I K + +F + +E +R+ T+ + + NP L N+ Y++
 Sbjct: 233 KIINEILSKEYLLFKVDYLNDYLEKNLKRFNSIKENQDLISRVARNPIQKLSKNERYFLI- 291

Query: 277 AGNKNSYIKLKKDSPVGIELTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVR 336
 Y +KK + +IL Y+ ++ + + + S QS ++ +
 Sbjct: 292 -----YNLVKKHNLEIDILLEI-----YKSIFYYDNKMDKESSKIQSTIEN--K 333

Query: 337 KEDYIYLDFFNLNQE 351
 Y F NL+QD
 Sbjct: 334 SLAYALKKFSNLDQE 348

tr Q8ID18	Hypothetical protein MAL13P1.349 [MAL13P1.349]	2170
Q8ID18_PLAF7	[Plasmodium	AA
	falciparum (isolate 3D7)]	<u>align</u>

Score = 39.3 bits (90), Expect = 0.19
 Identities = 53/261 (20%), Positives = 101/261 (38%), Gaps = 50/261 (19%)

Query: 3 NKYLKТИMPFDLSIYTNTDILIEFMNKYNSEXXXXXXXXRYKD-NNLIDLSGYGAKVE 61
 N + + F+ + + N+ LI+M NK N + NN+ +++ +
 Sbjct: 773 NSRMIYLOKFNSNFFENNFDLIDMKNKNNNINTNNVNNMDNMNNINNNINNINTNNVNNI 832

Query: 62 YDGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIH 121
 + LN+ N +TS+ N+K + + +N + N + L
 Sbjct: 833 NNVNNLNNINNSNITSNTNNKKYDESENSLHNILL-----K 870

Query: 122 NEYTIINCMKNNSGW---KISIRGNRIIWTLIDINGTKSVFFEYNIREDISEYINRWFF 178
 N T+ NC+ N+ GW KI + + + + I +F E +DI+E I
 Sbjct: 871 NFETVFNCVPND-GWITNKIDDEDENMLFYILHI---FELFVEIYEDKDINEII---- 920

Query: 179 VTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNT 238
 + N + +N + +D+K V IT K+ + + KY S+
 Sbjct: 921 -----IKNIVFFLN-----HTDLKIFSIVT---RIIIKISQINPINRIFFNKYISVLMK 966

Query: 239 ELSQSNIEERYKIQSYSEYLK 259
 + + + SY +Y K
 Sbjct: 967 NFDKDRRRNIFLMLSYCKYEK 987

Score = 39.3 bits (90), Expect = 0.19
 Identities = 67/315 (21%), Positives = 123/315 (38%), Gaps = 69/315 (21%)

Query: 50 IDLSGYGAKVEVYDGVELNDK-----NQFKLTSSANSKIRVTQNQNIIFNSVFLDFSV 102
 Sbjct: 90 IGWSNLASLKKFFENVKLKEKAQIICFENGYKISSFFQSILNIDSNH-----FVNASV 142

Query: 103 SFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFE 162
 Sbjct: 143 DKII--PNFKSDSLDVYVESYYEIIILEQKNESQKKLNF----- 178

Query: 163 YNIREDISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDI 222
 Sbjct: 179 VNYSTDLEAYINKKLFLV---NAIHSTIGYLGYLKKT---YINEALNDQQILFKIKRLA 232

Query: 223 DRTQFIWMKYFSIFNTELSQSNE---ERYKIQSYSEYLKDFWGPNP---LMYNKEYYMFN 276
 Sbjct: 233 KIINEILSKEYLLFKVDYLNDYLEKNLKRFSIKENQDLISRVARNPPIQKLSKNERYFLI- 291

Query: 277 AGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVR 336
 Sbjct: 292 -----YNLVKKHNLIEDILLEI-----YKSIFYYDNKMDKESSKIQSTIEN--K 333

Query: 337 KEDYIYLDFFNLNQE 351
 Sbjct: 334 SLAYALKKFSNLDQE 348

tr	<u>Q8ID18</u>	Hypothetical protein MAL13P1.349 [MAL13P1.349]	2170
	<u>Q8ID18_PLAF7</u>	[Plasmodium	AA
		falciparum (isolate 3D7)]	<u>align</u>

Score = 39.3 bits (90), Expect = 0.19
 Identities = 53/261 (20%), Positives = 101/261 (38%), Gaps = 50/261 (19%)

Query: 3 NKYLKТИMPFDLSIYTNDTILIEMFNKYNSEXXXXXXXXXRYKD--NNLIDLSGYGAKVEV 61
 Sbjct: 773 NSRMIYLQKFNSNFFENNFDLIDMKNNKNNINTNNVNNMDMNMMNNINNNINTNNVNNI 832

Query: 62 YDGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIH 121
 Sbjct: 833 NNVNNLNNINNSNITSNTNNKKYDESENSLHNILL-----K 870

Query: 122 NEYTIINCMKNNSGW---KISIRGNRIIWTLIDINGKTKSVFEEYNIREDISEYINRWFF 178
 Sbjct: 871 NFETVFNCVPND-GWITNKIDDEDENMLFYILHI---FELFVEIYEDKDINEII---- 920

Query: 179 VTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNT 238
 Sbjct: 921 -----IKNIVFFLN----HTDLKIFSIVT---RIIIKISQINPINRIFFNKYISVLMK 966

Query: 239 ELSQSNIIEERYKIQSYSEYLK 259
 Sbjct: 967 NFDKDRRNIFMLSYCKYEK 987

Database: EXPASY/UniProtKB
Posted date: May 10, 2005 1:53 PM
Number of letters in database: 613,355,151
Number of sequences in database: 1,906,987

Lambda K H
0.319 0.138 0.414

Gapped

Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

length of query: 465

length of database: 613,355,151

effective HSP length: 129

effective length of query: 336

effective length of database: 367,353,828

effective search space: 123430886208

effective search space used: 123430886208

T: 11

A: 40

X1: 16 (7.4 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 41 (21.7 bits)

S2: 76 (33.9 bits)

Wallclock time: 8 seconds

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Database: EXPASY/UniProtKB
Posted date: May 10, 2005 1:53 PM
Number of letters in database: 613,355,151
Number of sequences in database: 1,906,987

Lambda K H
0.319 0.138 0.414

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
length of query: 465
length of database: 613,355,151
effective HSP length: 129
effective length of query: 336
effective length of database: 367,353,828
effective search space: 123430886208
effective search space used: 123430886208
T: 11
A: 40
X1: 16 (7.4 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 41 (21.7 bits)
S2: 76 (33.9 bits)

Wallclock time: 8 seconds

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